O'Bryen, Barbara

From:

Switzer, Juliet

Sent:

Thursday, December 18, 2003 8:37 AM O'Bryen, Barbara

To: Subject:

please search

09/889491

please search seq id no 13 and 14 in all prior art databases. please also search in reg file in oligos of 100 or fewer crossed as appropriate with alignments. Thanks.

Juliet Switzer Art Unit 1634 703 306 5824 office CM1 12D15 mailbox CM1 12E12

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OM nucleic nucleic search, using sw model

December 18, 2003, 09:02:17; Search time 1387.89 Seconds (without alignments) 913.783 Million cell updates/sec

Result ŏ

Score

Length

Run on:

Title: Perfect score: Sequence: US-09-889-491-14 31

Scoring table: Gapop 10.0 , Gapext 1.0 1 atagtgaaaacttgtgtaattatgaaatttt 31

2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl:*

em_htgo_hum: *
em_htgo_mus: *
em_htgo_other: * em_htg_mam:*
em_htg_vrt:*
em_sy:* em vi:*
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em htg mus:*

Pred. No. 18 the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222222222 DB AC131872 AF538602 CEY69H2 AC116984 AC021301 AC021489 AC021489 AC021621 AC021621 AC021621 AC130840 AC080138 AC003264 AC003264 AC003864 BX005265 AC096365 AC017031 AC139706 AC141436 AC096386 AC017075 AC0252811 AC125548 109554 Hamo sapian Ac939460 Homo sapian Ac939044 Homo sapian Ac930044 Homo sapian Ac930044 Homo sapian Ac930044 Homo sapian Ac9303768 Homo sapian Ac9303768 Homo sapian Ac9303768 Homo sapian Ac930376 Homo sapian Ac930377 Rattus mo Ac930377 Rattus mo Ac930377 Homo sapian Ac930377 Hom Description AX028511 Sequence Human bone

JOURNAL,	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX028511	XESOPT I
Patent: WO 0042216-A 14 20-JUL-2000;	Genetic predisposition	Kusk, P.	P	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.	Homo sapiens	Homo sapiens (human)		AX028511.1 GI:10189694	AX028511	14 from Patent WO0042216.	AX028511 31 bp DNA linear PAT 16-SEP-2000		

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SOURCE
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                                                                                                         Homo sapiens bone sialoprotein L09554
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                                                 Homo sapiens (human)
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Kim,R.H., Shapiro,H.S., Li,J.J., Wrana,J.L. and
Characterization of the human bone sialoprotein
 Kerr, J.M., Fisher, L.W., Termine, J.D., Wang, M.G., McBride, O.W.
              Sukaryota, Metazoa, Chordata, Craniata, Verrebrata, Buteleostomi,
Mammalia, Eubheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 1221)
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Matrix Biol. 14 (1), 31-40 (1994)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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2179. .2260
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(BSP) gene and
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1 (bases 1 to 2461)
Kiyoshima, T., Yamauc
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1 ATAGTGAAAACTIGTGTAATTATGAAATTTT
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of Toronto, Room 234, 150 College:
Location/Qualifiers
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Kiyoshima, T. and Sodek, J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genomics 17 (2), 408-415 (1993)
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2052. .2056
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Location/Qualifiers
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note="G00-118-889"
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                                                                                                                                                             Submitted (14-728-2001) Whitehead Institute/MIT Conter
Research, 200 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1. (bases 1 to 78036)
Birren, B., Linton, L., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone CTD-2363K13
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AC090084
AC090084.1 GI:12830225
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: sequence submissions@genome.wi.mit.edu
                                                                                                              Center: Whitehead Institute/ MIT Center
                                                       Web site: http://www-seq.wi.mit.edu
                                                                                       Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/gene="IBSP"
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Pred. No. 5.3;
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Genome Res. 8 (11), 1097-1108 (1998)
99063792
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2 (bases 1 to 187624)
Harkins, C., Kozlowicz, A.
                                                                                                     Bukaryota, Metazoa, Chordata,
Mammalia; Eutheria; Primates,
1 (bases 1 to 187624)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                              AC093768 AC021959
AC093768.3 GI:16
                                   9847074
                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                 Homo sapiens BAC clone RP11-113G13 from 4, complete sequence.
                                                                                                                                                                                                                                                                                    AC093768
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22977
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2 422: gap of 100 by
3 12464: combig of 10042 by in length
5 12564: gap of 100 by
5 78036: combig of 65472 by in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
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/clone_lib="CITD Human BAC"
l. .2322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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     and Doebber, A.
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Sequence derived from one plasmid subclone, base position 69516 69532.
                                                             NEXIGHEORING SEQUENCE, INFORMATION;
The clone sequenced to the right is AC087106. Actual s
clone is at base position 1 of RP11-113G13; actual end
position 187624 of RP11-113G13.
                                                                                                                                                                                                                             SOURCE LIMPORMATION:
The RECT-11 human BAC library was made from the blood of one male donor, as described by Oscogawa K. Roon, P. Y. Zhao, B. Trengen, E. Tateno, M. Catansses. J. J. and de Jong, P. J. (1999) Man improved approach for construction of bacterial artificial normations approach for construction of bacterial artificial obstained exhibst from libraries, desmonice $11.48. The cions may be obstained exhibst from Research Genocios, Inc., (http://www.resgen.com) or Fater de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                        MAPPING IMPORMATION: Mapping information for this clone was provided by Dr. John D. Mapping information for this densition about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all regions were double stranded, sequenced with an alternate chemistry, or cowered by high quality data (i.e., phred quality > 30), an altempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly west confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as compressions and repeats;
from more than one subclone;
restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-MAR-2002) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-MAR-2002)
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                                                                                                                                                                                           coworkers at http://www.chori.org
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/note="similar to
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oh73g11.s1"
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/note="similar to
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16337. .16436
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|5645. .15865
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/clone_lib="RPCI-11"
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/chromosome="4"
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AUTHORS
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(NID:g14503296)"
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To 2 (Dases I to 153586)

Baldwin, J., Barna, M., Beckerly, R., Boguslavkiy, L., Bouthgalter, B., Baldwin, J., Barna, M., Beckerly, R., Boguslavkiy, L., Bouthgalter, B., Baldwin, J., Barna, M., Beckerly, R., Boguslavkiy, L., Bouthgalter, B., Brown, A., Gastle, A., Colangslo, M., Collins, S., Collycore, A., Doyle, M., Cooke, P., Dakrellano, K., Dewar, K., Domano, M., Donelan, J., Doyle, M., Cooke, P., Dakrellano, K., Grant, G., Hagon, B., Hatchorl, N., Borton, L., Balagan, J., Gardyna, S., Grant, G., Hagon, B., Hatchorl, N., Borton, L., Balagan, J., Gardyna, S., Grant, G., Hagon, B., Hatchorl, N., Borton, L., Balagan, J., Laudmon, R., Grant, G., Hagon, B., Hatchorl, N., McBan, P., McCatter, A., McKernan, K., McGan, B., McCatter, M., McBan, P., McCatter, A., McKernan, K., McGan, J., McCatter, J., Walley, R., Roy, A., Santos, R., Severy, P., Stanger-Thomann, M., Schamori, A., Tolanas, J., Tesfaye, S., Titroll, A., Wassiliev, H., Vo, A., Wheeler, J., Wh, X., Santos, S., Titroll, A., Wassiliev, H., Vo, A., Wheeler, J., Wh, X., Myan, D., Ye, M.J., Zimmer, A. and Zody, M., Wheeler, J., Wh, X., Santos, S., Walley, B., Walley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with Patent: WO 0200928-A 1946 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Merazoa; Chordata,
Mammalia; Eutheria; Primates;
1 (bases 1 to 153586)
Birren, B., Linton, L., Nusbaum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX346875.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX346875 ... 7771 bp D
Sequence 1946 from Patent W00200928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and
Homo sapiens, clone RP11-28K18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS PHASE1; HTGS DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ріесев
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens clone RP11-28K18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX34687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  artificial sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAATAAAACTTATATAATTATAAAATTTT 3092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAGTGAAATTTGTATAATTATGAAATTTT 4680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAGTGAAAACTTGTGTAATTATGAAATTTT
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153586 bp DNA linear HTG 09-SEP-200
1-28K18, WORKING DRAFT SEQUENCE, 9 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics, 100% of reads Chemistry, Dye Terminator Big Dye; 100% of reads Chemistry; Dye Terminator Big Dye; 100% of reads Assembly progitty; 1100 bases at least Q40 Consensus quality; 11300 bases at least Q40 Insert size; 15200; agrace-pt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary dags between the contige are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hearch, 320 Charles Street, Cambridge, MA 02141, USA
Sep 9, 2000 this sequence version replaced gi:6649327.
repeats were identified dusing RepeatMasker:
Lt, A.F.A. & Green, P. (1996-1997)
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118561
143778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: 28_K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: L477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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/note="assembly_fragment"
                                                                                                                                                                                                                                                                       vector
                                                                                                                                                                                                                                                                                            Clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:9606"
                                      note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                    cione="RP11-28K18"
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118560: gap of 100 bp
143777: contrig of 25217 bp in length
143877: gap of 100 bp
153586: contrig of 9709 bp in length.
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of 31737 bp
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TITLE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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hes 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gindés Gord S. Goyette, M. Graham L. Grand-Bearre N.
Hagos B. Horton L. Halma, W. Likuv I. Johnson, R. Jonnes C.
Kamat, A., Karatas A., Kalis C., Lakcoque K., Lamazares R.,
Kamat, A., Karatas A., Kalis C., Lakcoque K., Lamazares R.,
Landers T., Lachoczky, Levins, R., Lindblad-Toh, K., Liu, G.,
MacCantry, M., Koßwan, B., Koßernan, K., Keldtin, J., Wensus, L.,
Kicharty, M., Koßwan, B., Koßernan, K., Keldtin, J., Wensus, L.,
Kicharty, M., Koßwan, E., Kognoori, J., Napoler, J., Napoler, J.,
Kognoori, J., Kognoori, J., Obmenil, P., Owell, D.,
Olymb, C., Komman, L.K., Comnoori, J., Obmenil, P., Owell, D.,
Olymb, C., Komman, J., Comnoori, J., Obmenil, P., Owell, D.,
Olymb, C., Komman, J., Kognoori, J., Charles, R., Schamer, S.,
Reman, J., Kosetti, M., Roy, A., Gartos, R., Schamer, S.,
Secham, J., Severy, P., Spencer, B., Stange-Thomann, M., Scojamovio, M.,
Strauss, M., Ghardes, J., Travis, N., Trajilio, J., Vassiliav, H.,
Vial, R., V., A., Wilson, B., Wilson, M., Wanal, D., & M.J., Young, G.,
Jaccet, Shumkaidan
                                                                                                                            Research, 200 Charles Street, Combridge, MA 02141, USA
3 (hases I to 15229)
Skirren, B., Nabbaum, C., Lander, E., Abouellei, A., Allen, M.,
Anderson, S., Arachchi, H.M., Barna, M., Bastten, W., Bloom, Y.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Charg, J., Choepel, Y.
Chlymore, A., Cook, A., (Cooke, P., Corum, B., Dekrellano, K.,
Chlymore, A., Cook, A., (Cooke, P., Corum, B., Dekrellano, K.,
Chlymore, A., Cook, A., (Cooke, P., Corum, B., Dekrellano, K.,
Chlymore, A., Cook, A., (Cooke, P., Corum, B., Dekrellano, K.,
Parts, J., Border, J., M., Gose, D., Galagan, J., Gardyna, S.,
Ferreira, P., Fizcherald, M., Gose, D., Galagan, J., Gardyna, S.,
Graham, J., Gardyna, S.,
Hall, J., Herton, L., Hulber, M., Hiter, Y., Johnson, J., Bones, C.,
Hall, J., Kartstei, M., Kelle, J., Landers, Y., Levine, R.,
Lender, J., Kartstei, J., Kelle, J., Landers, Y., Levine, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (Dases i to 15522)

Birren, B., Linton, I., Nubbaum, C., Lander, E., Ali, A., Allen, N.,
Barten, B., Garten, L., Sastien, Y., Bloom, F., Sanderson, S., Sanderson, S., Sanderson, S., Sanderson, S., Congo, J.,
Bouklggiler, B., Brown, A., Comareta, J., Composition, A., Change, J.,
Characo, G., Choppel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cook, P., Debrellano, K., Dewar, K., Diasay, S., Dodge, S.,
Cook, A., Cook, P., Debrellano, K., Dewar, K., Diasay, S., Dodge, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, D., Galagan, J., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, D., Galagan, J., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, D., Galagan, J., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, D., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, D., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, D., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, D., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, G., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, G., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, G., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, G., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, G., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, G., Gardyna, S.,
Faro, S., Ferraira, P., Fizziugh, W., Gage, G., Gardyna, S.,
Faro, S., Faro, G., Fizziugh, W., Gage, G., Gardyna, G., Gardyna, S.,
Faro, S., Faro, G., Fizziugh, W., Gardyna, G., 
Lindbhad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarth
Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 155229)
Birren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC116813 155229 bp
Mus musculus clone RP24-357G23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-APR-2002) Whitehead Institute/MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus, clone RP24-357G23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46298 a
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clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
143878. .153586
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Pred. No. 2.1e+02;
0; Mismatches 5;
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       Matthews,C., McCarthy,M.,
lenga,V., Murphy,T., Naylor,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 153586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Choepel, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kguyen, C., Micol, R., Morbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oiler, J. P., Febreron, K., Phunbhang, P., Febrero, N., Senthahang, D., Saire, M., Sogov, P., Rachupka, A., Renasamy, U., Raymond, C., Retta, R., Sisse, S., Sitth, C., Roman, J., Schauer, S., Schupback, R., Seeman, S., Seeray, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubba, K., Talamas, J., Teakers, W., Talamas, J., Teakers, W., Telamas, J., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome
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consists of 4 contigs. Gaps between the contigs
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Sequencing vector; Dasmid; n/A; 100% of reads
Chemistry: Dye-terminator Hg Dye; 100% of reads
Assembly program; Drugn; version 0, 560731
Consensus quality; 154720 bases at least Q40
Consensus quality; 154977 bases at least Q20
Consensus quality; 154977 bases at least Q20
Tasert size: 154929; num-of-contigs
Quality coverage: 11.15 in Q20 bases; sgarcse-fp
Quality coverage: 11.15 in Q20 bases; sgarcse-fp
Quality coverage: 11.15 in Q20 bases; sgarcse-fp
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This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by the finished sequence as soon as it is available and the accession number will be preserved at 10 and 10
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Center clone name: 357_G_23
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FEATURES

FEATURES

be preserved.

43860: contig of 43860 bp in length 43960: gap of unknown length 165217: contig of 121257 bp in lengt

in length.

Quality coverage: 14.29 in Q20 bases; agarose-fp Quality coverage: 13.37 in Q20 bases; sum-of-contigs

MOTE: This is a "working draft" sequence. It currently commisses of 2 courties. The true order of the pieces is not known and their order in this sequence record is arbitrary, daps between the contists are represented as runs of M but the exact sizes of the gaps are unbrown. This record will be updated with the finished sequence as soon as it is available and the accession number will

source

organism="Mus musculus" Location/Qualifiers

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SOURCE
ORGANISM
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 165217)
McPherson, J.D. and Watt
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
Submitted (11-JWR-2003) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, W 63108, USA, On Jun 10, 2003 this sequence version replaced gi:22657849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC132362 165217 bp
Mus musculus chromosome UNK clone
                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                    Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                Wilson, R.K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 165217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                    Center project name: M_BA0455B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of Mus musculus clone
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                                                                                                                                                     Sequencing vector: M13; 0%
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Pred. No. 2.1e+02;
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     Overlapping Sequences:
5': Mapping in pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Box 352145, Seattle, WA 98195, USA
On Mar 28, 2002 this sequence version replaced gi:17975270.
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                                                                                  Sequencing vector: plasmid; 25% of reads
Sequencing vector: plasmid; 12% of reads
Sequencing vector: plasmid; 108752; 49% of reads
Chemistry; pye-primer EF; 25% of reads
Chemistry; pye-primer EF; 25% of reads
Chemistry; pye-terminotor EH; pye, 48% of reads
Chemistry; pye-terminotor EH; pye, 48% of reads
Assembly program: Phrap; version 0.990319
Consennus quality; 166421 bases at least Q40
Consennus quality; 166421 bases at least Q20
Consennus quality; 166421 bases at least Q20
Consenus quality; 166421 bases Q20
Consenus quality; 166421 bases at least Q20
Consenus quality; 166421 bases at least Q20
Consenus quality; 166421 bases at
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Submitted (21-DEC-2001) Genome Center, University of Washington,
now 377145. Seattle, MA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukarycta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butherta; Pfimates; Catarrhini; Hominidata; Homo. 1 (16868) 1 to 168433 Markey Y., James, R. A., Rouse, G., Rh.Z., Saarphimmachak, C., Phajps, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
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Center clone name: RP11-228H5 (bc0314)
Center clone name: Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: uwgchtgs@u.washington.edu
Drafting Center: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.genome.washington.edu
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Mapping in progress
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43961. .165217
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Pred. No. 2.1e+02;
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3': RP11-14301 (UWGC:bc0262) AC025817

Sequence Quality Assessment:

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

General filst filst format but are available as part This entry has been annotated with sequence quality

of this entry's ASN.1 file.

all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., but quality = 30), an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone, and the assembly was continued by restriction digest. This sequence was finished as follows unless otherwise noted: Phred

밁 8

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 by
are not resolved in the fingerprint and hence do not appear
in the vable. There are no significant remaining discrepancies
between the operational and predicted values. Uniquely ordered
fragments esparated by dashed lines.

BORI

BORI (approximately 400-800 bp.

5737	3260	5174	2649	6417	7817	8365	3111	346	9196	6260	2865	1852	818	355	1117	6	8696		SegDerMap	
5748	3283	5118	2696	6352	7818	8231	3138	<800	9141	6352	2911	1884	838	<800	1122	<800	8751		FngrPrnt	
542	2650	1194	2321	725	4175	3658	14916	223	2247	2988	6183	1009	2127	449	512	6382	2419	1	SeqDerMap	
<800	2660	1214	2308	<800	4079	3623	15066	<800	2308	3042	6195	1031	2104	<800	<800	6539	2464		FngrPrnt	
272	699	3491	6163	1215	458	1192	7	8407	2226	3685	4480	5081	4326	639	5089	2067	5987		SeqDerMap	
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		1113 672 8776 4512 7000	1866 8184 3178 1483	14779 5326 5038 5038 3043 3124 4499 785	2361 897 3865 614 166 62 237 3925 3926
		1122 <800 8751 4489 7039	<pre></pre>	14846 5118 5118 3138 3138 3138 4489 <800	2361 931 3915 <800 <800 <800 <800 2361 3138 3915
165 100 2639 3005	1402 853 2705 1718	7412 1885 657 1808	1368 2604 138 138 833 604	726 1439 . 2798 . 2798 . 5195 . 1227 . 2270	3101 4156 5463 1461 1314 462 462 820 820 853
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10607 1126 4989	3605	2756 1292 4807 9186	935 5425 1713 2219 3058	1315 3401 5066 80 498 498 3337 748	10526 708 11660 653 5442 1429 1129 1231 13263 5546
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1 1101: contig of 1101 bp in length 1102 1201: gap of unknown length 1102 2376; contig of 1175 bp in length 2377 2476; gap of unknown length 2477 3577; contig of 2901 bp in length 5378 5477; gap of unknown length 5478 7621; contig of 2166 bp in length 7624 7723: gap of unknown length	* consists of 21 continue to the pieces. * is not known and their order in this sequence record is arbitary, daps between the outlige are represented as "nums of N, but the exact sizes of the gaps are unknown. * fils record will be hypated with the finished sequence as soon as it is available and the accession number will be preserved.	Assembly program. Phrap, version 0,90019 Consensus quality, 16683 bases at least Q80 Consensus quality, 16683 bases at least Q80 Consensus quality, 16683 bases at least Q80 Consensus quality, 16680 bases at least Q80 Insert size, 185000, 20x008-fp Insert size, 175000, 10x000 bases, 10x000 Insert programs, 175000 bases, 10x000 Insert programs, 175000 bases, 10x000 Quality coverage, 5,7 in Q80 bases, 10x000-contigs Quality coverage, 1,11 in Q80 bases, 10x000-contigs		KENYONGHS HTG; HTGS PHASE; HTGS PAAPT. SOURCES Mrs musculus (house modise) ORGANISM Mrs musculus (house modise) EMERIYCE A Metazoa; Chordata; Craniata; Vertebrata; Buteloostomi; REPERRNCI (hasea Metazoa; Chordata; Sciurognathi, Muridae; Murinae; Mus. AUTHORS Mcherson, J.D. and Waterston, R.H. TITLE JOURNAL ORGANISM MRS. D. A. M. Waterston, R.H. REPERRNCI TO A MARCHANISM Clone REPERRNCI MRS. M. M. Waterston, R.H. TITLE JUNGATA ORGANISM MRS. D. A. M. WATERSTON, MRS. D. M. M. WATERSTON, MRS. D. M. M. WATERSTON, MRS. D. M. M. M. WATERSTON, MRS. D. M. M. WATERSTON, MRS. D. M. M. M. WATERSTON, MRS. D. M. M. M. WATERSTON, MRS. D. M. M. M. WATERSTON, MRS. D. M. M. M. WATERSTON, MRS. D. M. M. M. M. M. M. WATERSTON, MRS. D. M.	Query Match 174.2%; Score 23; DB 9; Length 168433; Bast Local Similarity 24.2%; Score 23; DB 9; Length 168433; Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Qy 1 ATROTECAMACTYTOTEMATENTGAMATTYT 31 Db 155208 ACASTGAMACKTYTTATATTYTATATTYT 155178 RESULT 13 AC130840 AL130840 chromosome UNK clone RP24-44364, WOKKING DEAFT DEFINITION Manuscalus chromosome UNK clone RP24-44364, WOKKING DEAFT DECOSSION AC130840; Conservation of T2519 bp DRA 11mear HTG 14-AUG-2002 DEFINITION Manuscalus chromosome UNK clone RP24-44364, WOKKING DEAFT DECOSSION AC130840; Conservation of T2519 bp DRA 11mear HTG 14-AUG-2002 DEFINITION MANUSCALL CONTROL OF TAXABLE C

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J8: gpp of unknown length
S579: contig of 4399 bp in length
S579: contig of k07913 bp in length
J9: contig of s777 bp in length
J9: contig of s777 bp in length
J9: contig of s7718 bp in length
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J9: 398 of unknown length
J9: contig of s7829 bp in length
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25428 .28981
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Best Local Similarity 83.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20817, USA On Nov 14, 2000 this sequence version replaced gi:10305191.
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Booketron-Sternberg, S. M., Benjamin, B., Blakesley, R. M., Guan, X., Pollager, G., Brinkley, C., Broose, S., Dietrin, S.-Q., Legaspi, R., Gupta, J., Boo, S. -L., 160, J., Karlins, S., Lee-Lin, S.-Q., Legaspi, R., Kcliskey, J.C., McCowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Styder, B., Stantripop, S., Thomas, J. W., Thomas, P. J., Tlongson, B. B., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M.A., Wetherby, K. D., Tang, J. -H. and Green, B. D.
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Quality coverage: 4.62x in Q20 bases; agarcse-fp
Quality coverage: 4.32x in Q20 bases; pulse-field-gel
Quality coverage: 4.38x in Q20 bases; sum-of-contigs
                                                              Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-reminator Big Dye; 100% of reads Assembly program. Phrap; version 0.990139 consensus quality; 167609 bases at least 040 consensus quality; 171224 bases at least 020 consensus quality; 171124 bases at least 020 insert size: 170000; agarses-fb least 020 insert size: 170000; agarses-fb-ded-gel meett size: 182000; pulse-fisad-gel meett size: 182000; pulse-fisad-gel meett size: 182000; pulse-fisad-gel
                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                               ----- Summary Statistics
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76020. .94737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig41"
128867. .173519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94838.
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36736 c 34663 g 50398 t
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94838. .128766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .66582
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Pred. No. 2.1e+02
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consists of 20 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown,
this record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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126781
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43742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL6/J"
    note="assembly_fragment"
                                                 /note="assembly_fragment"
                                                                                  .8405. .22402
                                                                                                      note="assembly_fragment"
                                                                                                                                                   'note="assembly_fragment"
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                                                                                                                                                                                                                                          9833. .12985
                                                                                                                                                                                                                                                          /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI mouse BAC library 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="RP23-361M18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26601: Banking of 4089 bp in ength
26701: gap of unknown length
30788: comking of 4088 bp in length
30888: gap of unknown length
30888: gap of unknown length
37889: gap of unknown length
43741: gap of unknown length
43741: gap of unknown length
51103: comking of 7565 bp in length
51103: gap of unknown length
52003: gap of unknown length
62003: gap of unknown length
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                                                                                                                               .18304
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gap of
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unknown
of 4099
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wn length
n bp in length
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bp in 1
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VERSION
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                                                     REFERENCE
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ORGANISM
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Best Local Similarity
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                                             Stituen, B., Famman, K., McKernan, K., Mharro, C., Musbaum, C.,
Cooke, P., Daly, M. J., Depayre, E., Devon, K., Dewar, K., DuRette, B.,
Cooke, P., Daly, M. J., Depayre, E., Devon, K., Dewar, K., DuRette, B.,
Cooke, P., Gage, D., Gensheimer, S., Geraigery, K., Gilmartin, T.,
Hagen, B., Halphen, I., Harris, K., Howhand, J. C., Huang, J., Hai, J.,
Hagen, B., Halphen, I., Harris, K., Howhand, J. C., Huang, J., Hai, J.,
Jacotor, L., Linton, L., MacKanies, J., Wagylats, B., McDormott, J.,
McGuntk, A., Holla, M., Norris, W., Morrow, J., Nachana, A., Naylor, J.,
O'Connor, T., Olotu, A., Peterson, K., Robetts, D., Rollins, G.,
Sarnaik, A., Shiu, P., Shyam, R., Stilwall, J., Shone, C.,
Sarnaik, A., Shiu, P., Shyam, R., Stilwall, J., Shone, C.,
Sarnaik, A., Shiu, P., Shyam, R., Stilwall, J., Shone, C.,
Strickland, C., Sydney, W., Tangl, T., Zemtseva, I., Zhao, J., and Zody, M.
Direct Shimiselon, C., Shone, C., Shone, C., Shone, C.,
Strickland, C., Sydney, W., Tangl, T., Zemtseva, I., Zhao, J., and Zody, M.
Direct Shimiselon, E., Shone, C., Shone, C., Shone, C.,
Strickland, C., Sydney, W., Tangl, T., Zemtseva, I., Zhao, J., and Zody, M.
Direct Shimiselon, E., Land, C., Shone, C., S
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Birren,B., Fasman,K., McKernan,K., Nusbaum,C., Richardson,P., Lander,E., Allen,N., Baker,J., Baldwin,J., Barna,N., Beckerly,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 17, clone hCIT54K19 Unpublished
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1 (bases 1 to 202233)
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AC003664.1 GI:2828774
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126781. .146139
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51204. .59905
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clone_end:SP6
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/note="assembly_fragment
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92492. .108668
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81202..92391
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35187 g 54911 t
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Pred. No. 2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richardson, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI 03-FEB-1998
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7-PE_LOUILY* "REAL" 10915: 11861 /TPL family* "MERSA" complement(13745: .14445) /TPL family* "LIPA16"	ment (9561, Eamily="MER77	Complement (89929065) /rpc family=MrRy7" /rpc family=MrRy7" Complement(91099560) /rpc family=MrRy7"	/ TPC LemnLy="Alusg" complement (7529. 8617) / TPC family="LINE2" / TPC family="LINE2"	complement (51735513) /rpt_family="AT_rich" 65726874	/rpc_family="LINE2" complement(5048. 5112) /rpc_family="Ar_rich"	/ Lyc_remity="A1icut; complement(4318. '4397) / Tyt_family="LINE2" / Tyt_family="LINE2" complement(4401. 4490.)	/rpt_family="AT_rich" 40864148	complement (3748. 3773) /rpt family="Ar_rich" 3828. 3892	/tpc_tentity=_Ai_ICH: /rpc_tentity==Ai ISG= /rpc_tentity==Ai ISG=	/rpt_family="J1" 30933158	complement (1977 2413) /rpt_family="MER28" 2794 2999	mplement(1447. pt_family="AT_	/map="17" /clone="holTf54X19" /clone=lb="Research Genetics/Cal Tech CITB978SK-B (plates 1-194)"	/OXYGAIASmm="HOMOD SEPISEDS" //mol_type="goronaic_DNN" //do_xref="faxon:9608" //db_xref="faxon:9608" //db_xref="faxon:97"	<pre>beats were identified using RepeatMasker: Smit, A.F.A. & p. (1996-1997) fctp.genome.washington.edh/RM/RepeatMasker.html. Locatton/Qualifiers 1. 202233</pre>	Direct Submission Submitted (10-79E-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, cambridge, MA (0241, USA On Feb J. 1998 This sequence wersion replaced gi:815559. The Stoden databases, finishing infromation, and all Chromatographic files used in the assembly of this clone are available from our anonymous fty site.	Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cooke, P., Daly, M.J., Depayre, B., Devon, K., Dewar, K., Dürkette, B., Etemadi, S., Ferreira, P., Forrest, C., Gage, D., Gardyna, S., Genshaimer, S., Geraigery, K., Gilmartin, T., Gray, D., Hagors, B., Harris, K., Horton, L., Hodand, J. C., Hail, L., Jacotock, L., Linton, L., McKenzie, J., Marquis, M., McEwan, P., McGurk, A., Meldrin, J., McKenzie, J., Marquis, M., McEwan, F., McGurk, A., Meldrin, J., Molla, M., Morris, M., McZwo, J., Mella, M., McKenzie, M., McZwo, J., McZwo, M., M., Meeler, J., McK., Ye, N.J., Zamasewa, I., Zhao, J. and Zody, M., M., Meeler, J., McZwo, M., McZwo, M., Zody, M., M., McEler, J., McKenzie, M., McZwo, M., Zody, M., M., McEler, J., McZwo, M., Zody, M., M., McEler, J., McZwo, M., McZwo, M., Zody, M., M., McEler, J., McZwo, M., McZwo, M., McZwo, M., McCannello, M., McCannello, M., McCannello, M., Zody, M., McCannello, M., McCannello, M., McCannello, M., McCannello, M., McCannello, M., Zody, M., McCannello, M., McCannello, M., McCannello, M., McCannello, M., Zody, M., McCannello, M., McCannello, M., McCannello, M., McCannello, M., Zody, M

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PEATU

COMME TIT

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Matches 26; Conservative 0; Mismatches 5; Indels 0
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Search completed: December 18, 2003, 09:50:15 Job time: 1396.89 secs

=> fil reg; d que 13 FILE 'REGISTRY' ENTERED AT 09:22:13 ON 18 DEC 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2003 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

17 DEC 2003 HIGHEST RN 627482-61-5 STRUCTURE FILE UPDATES: DICTIONARY FILE UPDATES: 17 DEC 2003 HIGHEST RN 627482-61-5

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2003

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at: http://www.cas.org/ONLINE/DBSS/registryss.html

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ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN

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RELATED SEQUENCES AVAILABLE WITH SEQLINK STN Files: GENBANK

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290212-92-9 REGISTRY

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RELATED SEQUENCES AVAILABLE WITH SEQLINK

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ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN T.3

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Page 2

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RELATED SEQUENCES AVAILABLE WITH SEQLINK

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L3 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN

RN 286027-92-7 REGISTRY

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RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

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FILE 'CAPLUS' ENTERED AT 09:22:48 ON 18 DEC 2003
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FILE COVERS 1907 - 18 Dec 2003 VOL 139 ISS 25 FILE LAST UPDATED: 17 Dec 2003 (20031217/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:493707 CAPLUS

DOCUMENT NUMBER: 133:130737

TITLE: Genetic predisposition to abnormal calcification

condition such as osteoporosis

INVENTOR(S): Kusk, Philip

PATENT ASSIGNEE(S): Osteometer Biotech A/S, Den.

SOURCE: PCT Int. Appl., 70 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

LANGUAGE: English FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

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WO 2000-EP319
     WO 2000042216 A2
                           20000720
                                                          20000117
     WO 2000042216 A3 20001102
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            MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
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PRIORITY APPLN. INFO.:
                                       GB 1999-1037
                                                      A 19990118
                                       GB 1999-12585
                                                      A 19990528
                                       WO 2000-EP319
                                                      W 20000117
    Methods of assessing an individual's predisposition to abnormal
     calcification conditions such as osteoporosis by detq. the genotype of a
    promoter for the bone sialoprotein gene, the matrix gla protein gene, the
    osteoponting gene or the osteoprotegerin gene individually or in any
    combination. Specific allelic variations for each promoter are described.
    286027-92-7 286027-93-8
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(unclaimed nucleotide sequence; genetic predisposition to abnormal

FILE 'HOME' ENTERED AT 09:22:55 ON 18 DEC 2003

calcification condition such as osteoporosis)

RL: PRP (Properties)

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search,

December 18, 2003, 09:02:17; Search time 203.279 Seconds (Without allignments) 411.664 Million cell updates/sec

using sw model

Perfect score: Sequence: 31 1 atagtgaaaacttgtgtaattatgaaatttt 31 US-09-889-491-14

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

N Geneseq 19Jun03:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21.6	21.6	21.6	22.6	23	27.8	31	31	Score
69.7	69.7	69.7	72.9	74.2	89.7	100.0	100.0	Query Match Length
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22	20	20	25	24	24	21	21	1 DB
AAK90942	AAX61629	AAX61630	ABX26253	ABL33973	ABL33972	AAA61936	MA74858	ID
Human digestive sy	B. burgdorferi ant	B. burgdorferi ant	_	Human immune syste	Human immune syste		Human bone sialopr	Description

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20	20	20	20	20	20	20.2	20.4	20.4	20.4	20.6	20.6	20.6	20.6	20.6	21.2	21.2	21.4	21.4	21.4	21.4	21:4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.6	21.6	21,6	21.6		21.6	21.6
64.5	64.5	64.5	64.5	64.5	64.5	65.2	65.8	65.8	65.8	66.	66.5	66.5	66.5	66.5	68.4	68.4	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.0	69.7	69.7	69.7	69.7		69.7	69.7
10945	6682	6682	6098	4705	3562	8846	9814	5163	578	89024	6227	6227	3959	3708	6863	2606	1503900	1503900	1503841	1503841	19634	19634	3747	2704	1474	1093	455	300	910715	111309	13377	13377	7737	7737	7737
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ALIGNMENTS

RESULT 1 AAA74858 ID AAA:

AAA74858 standard; DNA; 31 BP

17-JAN-2001 AAA74858; (first entry)

Human bone sialoprotein gene promoter BSP-G1869A polymorphic site.

Human; bone sialoprotein; BSP; bone mineral density; atherosclerosis; osteoporosis; promoter; ds.

Homo sapiens.

variation Location/Qualifiers replace(16,A) /*tag= a

/note= "BSP-G1869A polymorphism"

WO200042216-A2.

20-JUL-2000.

17-JAN-2000; 2000WO-EP00319

18-JAN-1999; 28-MAY-1999; (OSTE-) OSTEOMETER BIOTECH AS 99GB-0001037.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                          Novel therapsutic agent for prevention and treatment of calcified tumors and proliferative disorders such as esteosarcoma, multiple myeloma and breast cancer, comprises bone sialoprotein promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteotropic tumour; calcification; prostate tumour; osteosarcoma;
metaetatic tumour; hung breast; colon; brain; multiple myeloma;
benign prostatic hypertrophy; BPH; arteriosclarosis; osteospanesis;
osteoblast; bone repair; reporter construct; thromosome 4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bone sialoprotein promoter; BB9; human; tissue-specific promoter; targetted expression; therapeutic gene; toxic gene; gene therapy; osteotropic tumour; calcification; prostate tumour; osteosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assessing predisposition to a calcification condition etatus such as obteoporous a and atherosclerous, comprising determining the genotype of the promoter of the bone sisloprotein, matrix gla protein,
                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-442489/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone sialoprotein (BSP) promoter (-2184-+237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31 BP; 12 A; 1 C; 5 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteopontin or osteoprotegerin gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koeneman KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1999;
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Pred. No.
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c mammalian teletes to a novel gene therapy composition comprising a mammalian home saidoprotein (msp) promoter operably linked to a gene casespence encoding a toxic and/or therapeutic protein contained within a conditional content of the promoter directs gene expression in tissue and tumour cells with containing the content operable. It is active in fully-differentiated osteoblasts in home, in trophoblastic cells of the placenta, and in cementum and continue the test. It is also active in a viriety of human tumours or menisjonant growths which exhibit the sability to catching either in the menisjonant growths which exhibit the sability to catching either in the menisjonant growths which exhibit the sability to catching either in the majorant operation of the invention may be used to treat operation. It is also active in the promoter may also be expressed in non-malignant conditions in which calcification occurs, such as being composition of the invention may be used to treat oscentrally a protest may also be expression of a gene emoding a protein such as the property and expression of a gene genocing a protein such as provided the protein control of the protein control protein such as a composition of a gene genocing a protein such as a composition of a gene conding a protein such as a composition of a gene conding a therapeut to separate to protein such as a control of gene of the protein such as a control of gene to the such as a colony standard protein such as a such as a such as a colony standard protein such as a such as a such as a colony standard protein such as a colony standard protein such as a suc
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Sequence 2421 BP; 891 A; 438 C; 425 G; 667 T; 0 other;

Matches Query Match **LOCAL** Similarity Conservative 100.0%; Score 31; 100.0%; Pred. No. 0, Mismatches 0.094; DB 21; 0, Length 2421; ٥, Gaps

0

밁 S 1860 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31 ATAGTGAANACTTGTGTANTTATGMAATTTT 1890

RESULT 3 ABL33972 ID ABL

ABL33972 standard; DNA; ₽₽

(first entry)

Human immune system associated gene SEQ ID NO: 1945.

Human; immune system disease; cytosine methylation; antiastimatio; antiasteriosclawottic; antianaemic; cytositeic; nototropic; antianteriosclawottic; antianaemic; cytositeic; nototropic; antirihematic; antiarthitic; antianticonvolusant; ophthalmological; antirihematic; antiarthitic; antidiabetic; antipociatic; antiantiammatory; cancer; cyto disease; arteriosclarosis; anaemia; anune mysloid deukaemia; Alikiemer's disease; Alib; spilepsy; neurofibromatosis; rhematodid arthitis; poortiasis; bowed disease;

gene;

Homo sapiens.

WO200200928-A2

02-JUL-2001; 2001WO-EP07537.

30-JUN-2000; 2000DB-1032529. 01-SEP-2000; 2000DE-1043826.

(EPIG-) EPIGENOMICS AG

Claim 5; Fig 8A-B; 79pp; English

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RESULT 4
ABL33973/c.
ID ABL339
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective; anti-HIV; anti-tomvulsant, ophthalmological, anti-theumatic, anti-tarthritic, anti-tabetic, anti-postatic, anti-tarthritic, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 1946.
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                                                                       cytosine
                                                                                                     Nucleic acid comprising fra-
for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
01-SEP-2000;
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                                                                       methylation
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2000DE-1043826
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                                                                                                     fragment of chemically modified nent of diseases associated with
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                                                                                                                              useful
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gones which are modified by the methylation of cytosines. The sequence can be used in the diagnosts and treatment of immune system discorders, including eye diseases such as retinopathy, necvascular glaucoma and macular degeneration, arterinocalexonis, namenia, conner, acute mysloid betkeenia, Alabaimer's disease, AIDS, cpilepsy, neurofibromatosis, Themmatoid arthritis, peoriasis and inflammatory/ulcerative bowel themmatos.
                                                                                                                                                                                                                                                                                                                                         The present
                                                                                                                                                                                                                                                                                                                                         invention provides a number of human immune system associated
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Sequence 7771 BP; 2143 A; 45 C; 1537 G; 4046 T; 0 other;
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Matches
       Query Match
Best Local Similarity
 Conservative
        83.9%;
 0
        Pred.
               Score
 Mismatches
        No.
 5
               Length 7771
 Indels
 0
Gaps
 0
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3122 ATAATAAAACTTATATAATTATAAAATTTT
                                      ATAGTGAAAACTTGTGTAATTATGAAATTTT
                                         μ
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문 S

ABX26253 standard; CDNA; 134 BP

ABX26253

11-FEB-2003 (first entry

Human GDP-mannose 4,6-dehydratase (GM4, 6D) DNA #8310

arthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; manunosuppressive; antilnfiammatory; antiarthritic; antibacterial; cerebroprotective; Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant reje antiasthmatic; vasotropic. transplant rejection,

Homo sapiens

US2002110548-A1

11-JUN-2001; 2001US-0878574.

22-NOV-1996; 03-DEC-1997; 09-BEF-1998; 14-JUN-1999; 96US-0753233. 97US-0984246. 98US-0149674. 99US-0333177.

(GEMY) GENETICS INST INC.

Sullivan F, Kriz R, Kumar R;

New composition comprising ONP-mannose 4,6-dobydratase (AH,5D) peptide, for mannfacturing complex carbobydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transp.

transplant

Disclosure; SEQ ID NO 8312; 6pp; English

rejection

RESOULT PARTY NEW PARTY NE The invention relates to a composition comprising a human GDP-manuset 4,6-dailydratas (GM, GD) peptide. The peptide is useful for reducifying GM4, GD inhibitors, GM4, GD inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ampliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation graphylation (glycoconjugates. These diseases include architects. transplant rejection, asthma, sepsis, repertusion injury, stroke or infection. The GM4, ED peptide or a polymentectide encoding it is also useful for manufacturing complex carbobytrates and as targets for screening small nodecule antagoniers of the activity of the anaryme. The

Claim 1;

SEQ ID NO 1946; 32pp + Sequence Listing; German

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RESULT 6
AAX61630/c
ID AAX616
     Query Match
Best Local S
Matches 24
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Matches 25
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                 This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The bb polypeptides can be used in vaccines for cliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme discusse in immans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymucleotide is useful in developing an assay for defects in the suryme, as well as in gene replacement therapy, Sequences and ARXI7942-ARXI7944 and ARXI7947-ARXI3716 represent DNA molecules encoding human GM4,60 peptides of the invention.

Once The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USFTO at sequence you've sequence-halm.
                                                                                Sequence 615 BP; 212
                                                                                                                                                                                                                                                                                                       New isolated Borrelia burgdorferi nucleic acids - used to develop
products for the diagnosts, prevention and treatment of diseases
caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. burgdorferi antigenic protein
                                                                                                                                                                                                                                                                      Claim 1; Page 124; 275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic protein; vaccine; Lyme disease; infection; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999
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97US-0050359.
97US-0053344.
97US-0053377.
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                       69.7%;
85.7%;
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                                                                                A; 59 C; 98 G; 246 T; 0 other;
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Pred. No. 74;
                       Score 21.6;
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                                            DB 20;
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ATAATAAAAACTTATGTAATTATCAAAT
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RESULT 7
AAX61629/c
AAX616
                                                                                       AAX61629 standard;
                                19-JUL-1999
burgdorferi antigenic protein coding sequence,
                             (first entry
                                                                                       DNA; 654
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f739.nt.

Borrelia burgdorferi. Antigenic protein; vaccine; Lyme disease; infection; detection; ss.

HARKEX SXEXEX

밁 S

03-SEP-1997; 20-JUN-1997; 22-JUL-1997; 22-JUL-1997; (HUMA-) 18-JUN-1998; 30-DEC-1998. WO9859071-A1 MEDIMMUNE INC. HUMAN GENOME SCI INC 97US-0053377 9705-0053344 97US-0057483 97US-0050359 98WO-US12718

Choi GH, Brwin AL, Hanson . KS Lathigra

XXXXXXXXXX

REAL EXECUSION OF THE PARTY OF WPI; 1999-189980/16. P-PSDB; AAY19932.

New isolated Borrelia burgdorferi nucleic acids - un products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease used to develop ment of diseases

Claim 1; Page 124; 275pp; English.

This sequence encodes a Borrelia hungdorferi (Bb) protein of the invention, which is suitable for use in a waction. The Rp Daybeptides can be used in vactimes for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.

Sequence 654 BP; 227 A; 61 C; 104 G; 262 T; 0 other;

Matches Query Match Best Local Similarity 24; Conservative 69.7%; 0; Score 21.6; DB 20 Pred. No. 1.6e+02 Mismatches 20; 4. Indels Length 654; 0 Gaps

0

615 _ ATAGTGAAAACTTGTGTAATTATGAAAT 28 ATAATAAAAACTTATGTAATTATCAAAT 588

몆 8

RESULT 8 AAK90942

AAK90942 standard; DNA; 7737 먉

(first entry)

Human digestive system antigen genomic sequence SEQ ID NO: 4518.

Human; digestive system antigen; gene therapy; cancer; appendicitis;

Q

ATAGTGAAAACTTGTGTAATTATGAAAT 28

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Higestive coli digestive system Homo sapians. Homo sapians. Homo sapians. 17-JAN-2001 20 20-JAN-2001 20 21-JAN-2001 20
Homo mapiens: W020159314-N2.
Meckel's diverse
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25-88P-2000 27-88P-2000 27-88P-2000 29-88P-2000 29-88P-2000 29-88P-2000 29-88P-2000 29-88P-2000 20-001-2000 20-00
2000005-021449 2000005-021449 2000005-02149 200005-02169

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RESULT 9
AAS31977
ID AAS3
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AC AAS3
XX
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Best Local S
Matches 24
                   14 - IAM - 2000 | 2000 IIS - 0.179065 | 4 - FEB - 2000 | 2000 IIS - 0.18466 | 4 - FEB - 2000 | 2000 IIS - 0.18466 | 4 - FEB - 2000 | 2000 IIS - 0.18465 | 4 - FEB - 2000 | 2000 IIS - 0.18467 | 4 - FEB - 2000 | 2000 IIS - 0.18877 | 4 - FEB - 2000 | 2000 IIS - 0.18877 | 4 - FEB - 2000 | 2000 IIS - 0.18817 | 4 - FEB - 2000 | 2000 IIS - 0.18817 | 4 - FEB - 2000 | 2000 IIS - 0.28515 | 5 - FEB - 2000 | 2000 IIS - 0.295467 | 5 - FEB - 2000 | 2000 IIS - 0.295467 | 5 - FEB - 2000 | 2000 IIS - 0.295467 | 5 - FEB - 2000 IIS - 0.295467 | 5 - FEB - 2000 IIS - 0.295467 | 5 - FEB - 2000 IIIS - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 2000 III - 0.295467 | 5 - FEB - 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   divex associated protein human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; numnusuppressive; antarthetic; vasctropic, antarthematic; antiprolliferative; pyrostatid; cardiant; neuroprocentive; carebroprocective; moutropic, antibacterial; virunide, fungicide; cancer; ophthalmofrical; vulnerary; gene therapy, autoimmuse disease morphasm; physporollierative disorder; bease; live; cardivoraecular disease; dispersion; provided the same plasm; physporollierative disorder; bease; live; cardivoraecular disorder; dispersion; fungal infection; viral infection; colar disorder; beatcorder; disorder; gastrointestinal disorder; remal disorder; respiratory disorder; gastrointestinal disorder; remal disorder; respiratory disorder; provided the same plantation; tissue regeneration; anti-infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a number of human digestive system antiques. These can be used in the diagnosis, treatment and prevention of digestive system disorders; including cancer, Meckel's ediverticulum, bacterially sparsative infections, appendiatis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a general DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human liver associated genomic DNA #151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2001
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                                                                                                                                                                                                                                                                                                                              17-JAN-2001; 2001WO-US01351
                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200155355-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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2000US-0214886
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Pred. No. 1.
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24.4

20-OCT-2000; 2000US-0241786.

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05-DEC-2007, 2000US-0251030

05-DEC-2007, 2000US-0251981

05-DEC-2007, 2000US-0256719

06-DEC-2007, 2000US-025179

08-DEC-2007, 2000US-025185

08-DEC-2007, 2000US-025185

08-DEC-2007, 2000US-0251869

08-DEC-2007, 2000US-0251869

08-DEC-2007, 2000US-0251869
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08-NOV-2000;
08-NOV-2000;
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20-OCT-2000;
20-OCT-2000;
Sequences A831827-A832182 represent genomic DNA molecules, which encode the liver associated polypoptides of the invention. Liver associated polypoptides and their associated polymolecules are useful in the diagnosis, treatment and prevention of various types of discorders in e.g. humans, nice, rabbits, goats, lorses, cats, dogs, chickens or sheep. A puthological condition can be determined by detecting the presence absence of a mutation in a liver associated polymolecules. The treatable
                                                                                                 Claim
                                                                                                                      Isolated nucleic acid molecule encoding a human liver related protein is used in preventing, treating or ameliorating disorders of the liver particularly cancer of the liver
                                                                                                                                                                                                Rosen
                                                                                                                                                                         WPI; 2001-457728/49.
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                                                                                               1; SEQ ID No 453; 526pp; English.
                                                                                                                                                                                                                         HUMAN GENOME SCI
                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0244476
2000US-0244476
2000US-0244578
2000US-0244578
2000US-0244529
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2000US-0241808.

2000US-0241809.

2000US-0241817.

2000US-024617.

2000US-0246474.

2000US-0246475.
                                                                                                                                                                                                                                                                                                                                                                                   2000US-0250160
2000US-0250391
                                                                                                                                                                                                                                                          2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                Ruben
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Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                     disorders include autoimmune diseases such as rhewmatoid arthitis, bypeppoliferative disorders such as moplasms of the breast or liver, arthoroscular disorders such as cardiac artrest, cerebrovascular disorders such as cardiac artrest, cerebrovascular disorders such as cardiac, narvous system disorders such as Alaheiner's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as greenture labour and infertility, gastrointestinal disorders such as crobur's disease, remal disorders such as giomethosphitis mides can respiratory disorders such as sathma and pleurisy. The polypepides can also be used to aid wound healting; to prevent skin aging due to sumburn, omathmain organs before tramplantation, to responsate tissues and in the model.
                                                                                                                                             Note: The sequence data for this patent did not form part of the printed
Specification, but was obtained in electronic format directly from MIPO
at ftp.wipo.imt/pub/published_pct_sequences.
                             Local Similarity
24;
    Conservative
                             69.7%;
0;
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Pred.
    Mismatches
                             No. 1.
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Gaps
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4085 GTGAAACATTGTGTAATTACTAAATTTT 4112
                  4 GIGAAAACTIGIGIAAATTATGAAAATTIT 31
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0

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RESULT 10
ABK43114
ID ABK4:
  ABK43114 standard; DNA; 7737 BP.
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ABK43114; 21-MAY-2002 (first entry)

Genomic sequence #1013 encoding human connective tissue polypeptide

Human; commective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.

WO200155343-A1

17-JAN-2001; 02-AUG-200: 2001WO-US01322

11-JUL-2000 14-JUL-2000 26-JUL-2000 14-JUC-2000 14-JUG-2000 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 19-MAY-2000; 2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213. 2000US-0225214. 2000US-0225266. 2000US-0225267. 2000US-0217496. 2000US-0218290. 2000US-0220963. 2000US-0215135. 2000US-0216647. 2000US-0216880. 2000US-0217487. 2000US-0198123. 2000US-0214886. 200005-0209467. 2000US-0189874 2000US-0186350 2000US-0184664

2000US-0225447

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13-C27-2000
13-C27-2000
21-C27-2000
21-C27
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14-SEP-2000;
21-SEP-2000;
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08-SEP-2000;
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05-SEP-2000;
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29-SEP-2000;
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HUMAN GENOME SCI INC

Rosen Ş Barash SC, Ruben SK

WPI; 2001-565190/63

Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or Theumatoid arthritis -

Disclosure; SEQ ID No 2001; 673pp; English

The present invention relates to the isolation of novel human connective tissue related polyheptides (ANDS/613-ANDS/621) and the polyhenchectide (CDNA and genomic) sequences encoding them. The sequences of the invention are setfil in the diagnosis. Treatment, prevention and/or prognosis of diseases associated with connective tissue(s) including cancer. The polyhenchectide sequences of the invention are also useful in gene therapy. ANS/4116 typesent genomic sequences encoding the novel human connective tissue related polypeptides. Secuence are printed specification, but was obtained in electronic format directly from MIPO at the property of the printed specification, but was obtained in electronic format directly from MIPO at they have just publy published port. sequences.

Query Match Best Local S Matches 24 Sequence 7737 BP; 2397 A; 1325 C; 1490 G; 2525 69.7%; Score 21.6; DB 2 Pred. No. 1.5e+02 0; Mismatches DB 23; T; 0 other; Length 7737;

Similarity

24; 0, 4.

> 0 Gaps

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RESULT 11
ABN90332
05-SEP-2000;
08-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
27-SEP-2000;
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01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
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hepatitis; viral; parasitic; bacterial; fungal; inflammatory condi
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2000US-22945P.
2000US-229513P.
2000US-231413P.
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2000US-226868P.
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RESULT 12 AAS46476 ID AAS4

AAS46476 standard; DNA; 13377

BP

Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP,

Tumour suppressor gene derived chemically modified sequence #198

18-DEC-2001 AAS46476;

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Query Match Best Local S Matches 24

Similarity

69.7%;

Score 21.6; DB 24; Pred. No. 1.5e+02;

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Conservative

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Mismatches

4 GTGAAAACTTGTGTAATTATGAAATTTT 31

GTGAAACATTGTGTAATTACTAAATTTT 4112

Sequence 7737 BP; 2397 A; 1325 C; 1490 G; 2525 T; 0 other;

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01-NOV-2000;
17-NOV-2000;
08-DEC-2000;
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(RUBE/) RUBEN S M
(BARA/) BARASH S
                                                                                                                                                                                                                                                                                               citrinosis and graminomatous hepatitis), damage coised by drugs or toxini autoimmune diseases (e.g., adenomas, haemangiomas and hepatocollular carcinoma), portal hypertension, or gastrointestinal discorders (e.g., peptic ulcers, gastrititis and peritoneal diseases). Liver antigen polypeptides and polymedetides may also be used in errening for compounds which modulate liver antigen expression or activity. The polymentes the same for gene therapy, chromosome mapping, in the identification of individuals and in forense analysis, and the polymentes must be used as miscoular and the corporation of the polymentes of the control of the polymentes of the corporation of the control of the polymentes of the corporation of the polymentes of the polymentes of the corporation o
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                                                                              Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                           genomic sequences.
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at seqdata.uspto.gov/sequence/
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07-APR-2000;
30-JUN-2000;
                                                          ABL33463 standard; DNA; 13377
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                                                                                                                                                                                                                                                                                                                                                                                                     of the printed specification, but was obtained in electronic format directly from WIFO at
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                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent
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2000DB-1019173.
2000DB-1032529.
2000DE-1043826.
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85 7%;
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Mucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cyrosine methylation; antiasthmatic; antiasteriosclærict; protestic; artiastemics cyrosine methylation; antiasthmatic; antiastheriosclæric; protesticie; antiastheriosclæric; cyrosine cyrosine; antiastheriosclæric; antidisbatic; antiastheriosclærosis; antiastheriosclærosis; antiastheriosclærosis; antiastheriosclærosis; antiastheriosclærosis; protestic; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olek A,
Claim 1; SEQ ID NO 1436; 32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-BP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×
              German
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Query Match Best Local : The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the disgnosis and treatment of immune system disorders, including eye diseases under a retinopathy, neovescular glaucoma and macular degeneration, arteriosclerosis, maemia, cancer, acute myeloid leukaemia, Alleiner's disease, AIDS, spliepsy, henvofibroatenistics, returnancial arthritis, peoriasis and inflammatory/plecrative bowel intemmental arthritis, peoriasis and inflammatory/plecrative bowel Sequence 13377 BP; 3714 A; 146 C; 2702 G; 69.7%; 85.7%; Score 21.6; Pred. No. 1 6815 T; 0 other; Length 13377;

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4 GTGARARCTTGTGTRATTATGARATTTT 31
                   24;
                             Similarity
                     Conservative
                   0
                   Mismatches
                             .5e+02
                   ů
                   Gaps
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0,

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RESULT 14
AAX20250/c
ID AAX202
XX
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片 Q

GTGAAAATTTGTATAATTTTGAATTTTT 1854

Matches

AAX20250 standard; DNA; 111309 먉

BX8XBXBXBXBX8X8 04-MAY-1999

Borrelia burgdorferi polynucleotide sequence (first entry)

Borrelia burgdorferi, spirochete; hacterium, pathogen, lyme disease; epidemic relapsing fever; endemic relapsing fever; byme borreliosis; infection; disgnosis; characterisation; detection; ds.

WO9858943-A1 Borrelia burgdorferi

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RESULT 15
AAX20248/c
ID AAX202
XX
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Best Local S
Matches 24
                       03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AXXQUAR to AXXQAQO represent polymocleotide sequences isolated from Borrelia burgdorferi (Bb). Products desirved from Bb can be used for the descrition, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biopynthetic products, e.g. enzymes, Borrelia belongs to a family of motile, spiral-shaped batteria called Spirothetes spiral-shaped and borrelia causes epidemic and spiral-shaped batteria causes epidemic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Borrelia hurgdorferi muclaic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                              Borrella burgdorferi, spirochete; hacterium; pathogen; Lyme disease;
epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                04-MAY-1999
                                                                                                                                                                                                                                                                                                                                   AAX20248 standard; DNA; 910715 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 111309 BP; 35956 A; 13151 C; 19075 G; 43117 T; 10 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 738-800; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-081217/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDIAMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1998
(HUMA-) HUMAN
                                                                                          18-JUN-1998;
                                                                                                                    30-DEC-1998.
                                                                                                                                               WO9858943-A1
                                                                                                                                                                      Borrelia burgdorteri.
                                                                                                                                                                                                                                                     Borrelia burgdorferi polynucleotide sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                      102865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                (first entry)
GENOME SCI INC
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97US-0050359.
97US-0053344.
97US-0053377.
                         97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                          98WO-US12764.
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.6; DB 20;
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 111309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Search completed: December 18, Job time: 212.279 secs
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                AXX2024 to AXX20402 represent polymuclectide sequences isolated from Borrella burgdorferi (Bb) Products derived from Bb can be used for the detection, diagnoss, characterisation, prevention and therapy of Bb infections, e.g. type disease. They can also be used for the production of biosynthetic products, e.g. can rombe Spricohetes to a family of motiles partial shaped bacteria colled Spricohetes to a family of motiles product has been and bacteria colled Spricohetes Spricohetes are pathogolic in humans and borrella causes epidenic and endemity reduping fewer, and type borrellas causes commonly known as endemicing reduping fewer, and type borrellass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Borrelia burgdorferi mudeic acids - used to develop products for the detection, diagnosts, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayton R,
White OR;
                                                                                                                                                                                                                                Sequence 910715 BP; 327171 A; 129646 C; 130753 G;
                                                                                                                                                                                                                                                                    Lyme disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 157-671; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-081217/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEDI-) MEDIMMUNE INC
                                                                          692251 ATAATAAAACTTATGTAATTATCAAAT 692224
                                                                                                              1 ATAGTGAAAACTTGTGTAATTATGAAAT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dougherty BA,
                                                                                                                                                        Conservative
                                                                                                                                                                       69.7%;
85.7%;
                    2003, 10:30:05
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                                                                                                                                                        0;
                                                                                                                                                                          Score 21.6;
Pred. No. 1.
                                                                                                                                                        Mismatches
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                                                                                                                                                                          1.3e+02
                                                                                                                                                                                            DB 20;
                                                                                                                                                                                                                                   323091 T; 54 other;
                                                                                                                                                           Indels
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                                                                                                                                                        0;
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0

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 09:02:17; Search time 45,2395 Seconds (without alignments) 302:521 Million cell updates/sec

Title: Perfect score: US-09-889-491-14 31

Sequence: 1 atagtgaaaacttgtgtaattatgaaatttt 31

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

It issued_Patents_Nn;

11 / cgm2_6/podata/2/jna/Sh_coMB_seq;*

22 / cgm2_6/podata/2/jna/Sh_coMB_seq;*

33 / cgm2_6/podata/2/jna/Sh_coMB_seq;*

44 / cgm2_6/podata/2/jna/Sh_coMB_seq;*

54 / cgm2_6/podata/2/jna/Sh_coMB_seq;*

55 / cgm2_6/podata/2/jna/Sh_coMB_seq;*

66 / cgm2_6/podata/2/jna/Sh_coMB_seq;*

Pred. No. is the number of results predicted by chance to have a score ogeneter than or equal to the score of the result being printed, and is derived by analysis of the botal score distribution.

SUMMARIES

Query Match Length DB ID Match 1001 4 US-09-641-538-465 62.6 1001 4 US-09-641-538-466 62.6 1001 4 US-09-641-538-95 62.6 1002 4 US-09-641-638-95 62.6 1558 3 US-09-689-1	DB
	1
9764441	7771

Query Match

62.6%; Score 19.4;

DB 4;

Length 1001;

28 18.4 59.4 500 4 18-09-124-522-66 29 18.4 59.4 500 4 18-09-124-522-66 30 18.4 59.4 500 4 18-09-124-122-66 30 18.4 59.4 500 4 18-09-411-481-86 30 18.2 59.4 500 4 18-09-411-481-86 30 18.2 59.4 500 4 18-09-411-481-86 30 18.2 59.4 1300025 4 18-09-129-125-551 31 18.4 59.4 2451 4 18-09-328-5251 31 18.4 59.4 1300025 4 18-09-128-5251 31 18.2 59.7 137.9 18-09-128-125-179 32 18.2 59.7 137.9 18-09-128-125-179 33 18.4 59.4 1300025 4 18-09-128-125-179 34 18.2 59.7 177, 4 18-09-128-137-179 35 18.2 59.7 141.9 18-09-128-137-179 36 18.2 59.7 141.9 18-09-128-13-1 37 19.2 59.7 141.9 18-09-128-13-1 38 19.2 59.7 141.9 18-09-128-13-1 39 19.2 59.7 141.9 18-09-128-1
18.4 59.4 59.0 4 US-09-124-523-86 Sequence 18.4 59.4 59.0 4 US-09-515-7964-86 Sequence 18.4 59.4 59.0 4 US-08-615-7964-86 Sequence 18.4 59.4 59.0 4 US-08-611-968-96 Sequence 18.4 59.4 1581 4 US-09-528-525-255 18.5 59.4 1581 4 US-09-228-158-11 Sequence 18.4 59.4 1581 4 US-09-228-158-178 Sequence 18.5 59.7 17.7 4 US-09-528-1525-178 Sequence 18.2 58.7 17.7 4 US-09-528-178 Sequence 18.2 58.7 17.9 5 PCT-0893-0953-4 Sequence 18.2 58.7 17.9 4 US-09-61-4113-23 Sequence 18.2 58.7 17.9 4 US-09-623-1441-23 Sequence 18.2 58.7 17.9 1 US-09-528-144-1 Sequence 18.2 58.7 72.0 2 US-09-129-144-17 Sequence 18.2 58.7 72.0 3 US-09-129-144-17 Sequence 18.2 58.7 72.0 4 US-08-527-130-15 Sequence 18.2 58.7 72.0 4 US-08-528-10 Sequence 18.2 58.7 72.0 5 US-08-528-10 Sequence
\$9.4 500 4 US-09-124-523-86 Sequence 59.4 500 4 US-09-565-7966-86 Sequence 59.4 180 4 US-09-565-7966-86 Sequence 59.4 180 4 US-09-560-198-80 Sequence 59.4 1330026 4 US-09-526-525-15 Sequence 59.4 1330026 4 US-09-526-525-17 Sequence 59.7 1119 1 US-09-526-532-178 Sequence 59.7 1419 5 PCT-US39-09531-4 Sequence 58.7 1459 5 US-09-563-14 Sequence 58.7 1459 5 US-09-528-0532-13 Sequence 58.7 1459 1 US-09-523-0532-3 Sequence 58.7 1459 1 US-09-523-0532-3 Sequence 58.7 1459 5 US-09-523-0532-3 Sequence 58.7 1459 5 US-09-523-0532-3 Sequence 58.7 1459 5 US-09-563-141-10 Sequence 58.7 1459 5 US-09-563-611-10 Sequence 58.7 7210 5 US-09-563-6311-10 Sequence 58.7 7210 5 US-09-563-07301-10 Sequence 58.7 7210 5 US-09-563-07301-10 Sequence
500 4 US-09-124-523-86 Sequence 500 4 US-09-124-523-86 Sequence 500 4 US-08-431-048E-86 Sequence 151 4 US-08-601-198-80 Sequence 2451 4 US-08-601-198-80 Sequence 2451 4 US-09-228-352-2551 Sequence 132025 4 US-09-228-352-178 Sequence 132025 4 US-09-228-352-178 Sequence 1419 1 US-09-228-352-178 Sequence 1419 1 US-09-238-352-178 Sequence 1419 1 US-08-749-552-3 1456 4 US-08-749-552-3 1479 1 US-08-728-141-32 Sequence 1419 1 US-09-228-141-17 Sequence 1419 1 US-09-228-141-17 Sequence 1419 1 US-08-257-3414-17 Sequence 1419 1 US-08-257-3414-17 Sequence 1419 1 US-08-257-3414-10 Sequence
4 US-09-124-123-16 Sequence 4 US-09-124-123-16 Sequence 4 US-08-124-124-16 Sequence 4 US-08-124-124-14 Sequence 4 US-09-124-125-25-1 Sequence 4 US-09-124-125-17 Sequence 4 US-09-124-125-17 Sequence 5 EZT-US33-09631-4 Sequence 5 US-09-124-131-3 Sequence 6 US-09-124-131-3 Sequence 7 US-09-124-134-1 Sequence 7 US-09-123-134-1 Sequence 7 US-08-127-134-1 Sequence 8 US-08-127-134-1 Sequence 9 US-08-127-134-1 Sequence
4 US-09-124-123-16 Sequence 4 US-09-124-123-16 Sequence 4 US-08-121-1948-16 Sequence 4 US-09-124-1948-16 Sequence 4 US-09-124-1948-16 Sequence 4 US-09-124-1352-13 Sequence 4 US-09-124-1352-178 Sequence 5 E7T-US93-09634-4 Sequence 5 US-09-124-1311-3 Sequence 6 US-09-124-1311-3 Sequence 7 US-09-124-1314-1 Sequence 7 US-09-124-134-1 Sequence 7 US-08-257-134-1 Sequence 8 US-08-257-134-10 Sequence 9 US-08-257-134-10 Sequence
6 Sequence 6 Sequence 7 Sequence 8 Sequence 8 Sequence 9 Sequence 9 Sequence 9 Sequence 9 Sequence 9 Sequence 9 Sequence
86, Appl 86, Appl 86, Appl 87, Appl 88, Appl 88, Appl 89,
Appl Appl Appl Appl Appl Appli Appli Appli Appli Appl Appl

ALIGNMENTS

RESULT 1 US-09-641-638-465/c

Best Local Similarity

79.3%; Pred. No.

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US-09-641-638-595/c
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                                                                                                                                                                                                                                                                                               US-09-641-638-466
                                   GENERAL INFORMATION:
                                                 Sequence 595, Application US/09641638
Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 466, Application US/09641638
Patent No. 6432648
                                                                                                                                                                                                                             Matches
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  APPLICANT:
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PRIOR FILING DATE: 2000-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: upstream amplification primer, complement NAME/KEY: primer bind LOCATION: 164.183
OTHER INFORMATION: downstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KSY: misc_binding
LOCATION: 481..500
OTHER_INFORMATION: 12-44-67.misl, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TILE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TILE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 12-44-67 potential probe
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_binding
LOCATION: 489..513
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer bind
LOCATION: 547..567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 502..521
OTHER INFORMATION: 12-44-67.mis2, potential complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-44-67 : polymorphic base T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_binding
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                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           863 ATAGTTAGAAATTATCTAAATATGAAATT 835
                                                                                                                                                         880 ATAGTTAGAAATTATCTAAATATGAAATT 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATAGTGAAAACTTGTGTAATTATGAAATT 29
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                                                                                                                                                                                          ATAGTGAAAACTTGTGTAATTATGAAATT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bougueleret, Ly
Chumakov, Ilya
Bougueleret, Lydie
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                   Blumenfeld, Marta
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                                                                                                                                                                                                                             Conservative
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UMBER: US 60/133,200
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                                                                                                                                                                                                                                           79.3%;
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                                                                                                                                                                                                                                           Score 19.4;
Pred. No. 1.
                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                            Length 1001;
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US-09-286-691-1
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CURERNY APPLICATION WIMERE: U8/9/641,638
CURERNY PILLING DATE: 2000-08-16
PRICE FILLING DATE: 2000-08-13
PRICE FILLING DATE: 2000-02-11
PRICE APPLICATION WIMERE: U8 60/133,200
PRICE APPLICATION WIMERE: U8 60/133,200
PRICE APPLICATION WIMERE: U8 69/275,267
PRICE FILLING DATE: 1999-03-03
PRICE FILLING DATE: 1999-03-03
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LENGTH: 1002
                                                                                                                                       SEQ ID NO 1
LENGTH: 1558
                                                                                                                                                                                                                                                                                                                                                                               GENERAL IMPORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION. Cellulases
FILE REFERENCE: 42-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09286691
Patent No. 6190189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: PCT US97/18008
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/286,691
CURRENT FILLING DATS: 1999-04-05
EARLIER APPLICATION NUMBER: US 60/027,883
EARLIER FILLING DATE: 1996-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
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TITLE OF INVENTION: ELECTION CENES INVOLVED IN ARACHIDONIC ACID METABOLISM
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFFIRE INPOSMATION: 12-44-181.mis1, potential
NAMA/KEY: primer bind
LOCATION: 618-680: upstream amplification primer, complement
NAMA/KEY: primer bind
NAMA/KEY: primer bind
UCCATION: 25:.254
OFFIRE INPOSMATION: downstream amplification primer
                      FEATURE:
NAME/KEY: CDS
LOCATION: (105)..(1481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 488
OTHER INFORMATION: 12-44-181 : deletion
NAMEKENEY: misc binding
LOCATION: 438.457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                      ORGANISM: Orpinomyces sp. PC-2
                                                                                                                    TYPE: DNA
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les 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     951 ATAGTTAGAATTATCTAAATATGAAATT 923
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Pred. No. 1.1e+02;
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Query Match

62.6%;

Score 19.4;

DB 3;

Length 1558;

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                           PETICE APPLICATION INDMESS: US 66/126,903
PETICE PLATE: 1395-03-10
PETICE PLATE: 1395-03-10
PETICE PRIVATE PLATE: 1395-04-30
PETICE PRIVATE PLATE: 1395-04-30
PETICE PRIVATION INDMESS: US 66/132,065
PETICE PRIVATION INDMESS: US 66/142,928
PETICE PRIVATION INDMESS: US 66/143,928
PETICE PRIVATION INDMESS: US 66/143,928
PETICE PRIVATION INDMESS: US 66/145,915
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6476208
                                                                                                                                                                                  APPLICANT: ESSIOUX, LAUTENE
TITHE OF INVENTION: SCHIZOPHERNIA ASSOCIATED GENES; PROTEINS AND BIALLELIC MARKERS
FILE REPERBYCH: GENEST 047ANS
CHERBOT APPLICATION NUMBER: U5/09/539,333D
CHERBOT APPLICATION NUMBER: U5/09/539,333D
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CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/027,883
PRIOR FILING DATE: 1996-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER OF SEQ ID NOS
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LOCATION: (105)..(1481)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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APPLICATION NUMBER: US 60/146,452
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                FILING DATE: 1999-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09687147
                                                                                                                                                                                                                                                                                                         Blumenfeld, Mar
Chumakov, Ilya
                                                                                                                                                                                                                                                                         Bihain, Bernard
                                                                                                                                                                                                                                                                                            Bougueleret,
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Chen, Huizhong
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Pred. No. 1.1e+02;
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                                                                                Matches
                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEC ID NOS: 231
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                                                                                                                                                                                NAME/KEY: misc_binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-15065-85 probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
IOCATION: 1501
OTHER INFORMATION: 99-15065-85 : polymorphic base C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                       NAME/KEY: primer bind 
LOCATION: 1120..1140
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer bind
LOCATION: 1586, 1585
OTHER INFORMATION: upstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 99-15065-85.mis2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: 1481..1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRATURE:
NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 99-15065-85.misl, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_binding
LOCATION: 1502..1520
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   2059 AGTGAATAGTGGTATAAATATGAAAGTTT 2031
                                                                                                                                                                                                                                                                 INFORMATION: downstream amplification primer
                                                                                23;
                                      3 AGTGAAAACTTGTGTAATTATGAAATTTT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent.pm
                                                                                Conservative
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                                                                                                   62.6%;
79.3%;
                                                                                                   Score 19.4; DB 4; Length 3001;
Pred. No. 1.1e+02;
                                                                                   Mismatches
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                                                                                Gaps
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US-09-539-333D-216/c
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                                                                                     PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/143,928
                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/539,333D
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cohen, Daniel
                                                                                                                                                                                                                                                                                                    PELICANT: Essioux, Laurent
TILE OF INVENTION: SCHEOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC WARKS
TILE REFERENCE: GENEET.047AUS
                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT
APPLICATION NUMBER: US 60/146,453
                                     APPLICATION NUMBER: US 60/145,915
                                                                      FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 Bougueleret,
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                      1999-07-27
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PRIOR FILING DATE: 1999-07-29

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RESULT 8
US-09-345-882-1
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FERENAL INFORMATION:
APPLICANT: BAUDUNICA NACLEIC ACID ENCODING A RETINOBLASTOVA BINDING PROTEIN (REP-7)

TITLE OF INFUNCTION: A NACLEIC ACID ENCODING A RETINOBLASTOVA BINDING PROTEIN (REP-7)

TITLE OF INFUNCTION: A NACLEIC ACID ENCODING A SECULTED WITH SAID NUCLEIC ACID.

TILE REPERRICE: GRUET: 031A

CIREBRY PILITS OF THE SECULT ON UNMERS: US 00/09/345,882

TRICK PILITS DATE: 1998-06-30

PRICKS PILITS DAT
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SOFTWARE: Patent.pm
SEQ ID NO 216
LENGTH: 3001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.6%;
Best Local Similarity 79.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                   SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
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PRION FILING DATE: 1999-07-29 60/162,288
PRION FILING DATE: 1999-10-28
PRION FILING DATE: 1999-10-28
PRION APPLICATION NUMBER: US 09/416,384
PRION FILING DATE: 1999-10-12
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NAME/KEY: misc_binding
LOCATION: 1489...1513
OTHER INFORMATION: 99-27297-280 probe
                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer_bind
LOCATION: 1206..1224
OTHER_INFORMATION: downstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE: misc_binding
NAME/KEY: misc_binding
LOCATION: 1481..1500
OTHER_INFORMATION: 99-27297-280.mis1,
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NAME/KEY: allele
LOCATION: 1501
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      OTHER INFORMATION: 5-124-273 :
                                     NAME/KEY: allele
LOCATION: 72794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: upstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 99-27297-280 : polymorphic base T or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapiens
                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KBY: primer_bind
LOCATION: 1761..1779
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Pred. No. 1.1e+02;
polymorphic base
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NAME/KEY: allele LOCATION: 146345 COTHER INFORMATION: FEATURE:	HANDER : allele LOCATION: 146328 OTHER INFORMATION:	; FEALURE: ; NAME/KEY: allele ; LOCATION: 134374 ; OTHER INFORMATION:	NAME/KEY: allele LOCATION: 134362 OTHER INFORMATION:	MAME/KEY: allele LOCATION: 134134 COTHER INFORMATION:	; NAME/KEY: allele ; NAME/KEY: allele ; LOCATION: 108471 ; OTHER INFORMATION:	; FEATURE: ; NAME/KEY: allele ; LOCATION: 108308 ; OTHER INFORMATION:	; NAME/KEY: allele ; LOCATION: 108149 ; OTHER INFORMATION:	; MAME/KEY: allele ; LOCATION: 108106 ; OTHER INFORMATION:	; FEATURE: allele ; LOCATION: 106940 ; COTHER INFORMATION:	; FIGATURE: allele ; LOCATION: 103806 ; OTHER INFORMATION:	; NAME/KEY: allele ; LOCATION: 99117 ; OTHER INFORMATION:	MAME/KEY: allele ; LOCATION: 99098 ; OTHER INFORMATION:	; REATURE; allele ; NAME/KEY; allele ; LOCATION: 97152 ; OFHER INFORMATION:	; FEATURE; allele ; NAME/KEY: allele ; LOCATION: 97122 ; OTHER INFORMATION:	; NAME/KEY: allele ; LOCATION: 93714 ; LOCHER INFORMATION:	I MAME/KEY: allele I LOCATION: 90842 I OTHER INFORMATION:	; FEATURE: allele ; NAME/KEY: allele ; LOCATION: 88073 ; OTHER INFORMATION:
: 5-143-101 :	5-143-84 :	: 5-140-361 :	5-140-348 :	; 5-140-120 ;	5-136-174 :	5-135-357 :	5-135-198 :	5-135-155 :	5-133-375	5-131-395 ;	5-130-276 :	5-130-257 :	5-129-144 :	99-1442-224	5-128-60 ;	99-1437-325	5-127-261 :
polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphic	polymorphia	; polymorphic	polymorphic l	: polymorphic	polymorphic
base	base A	base	base	base	base	base	base	base	base	base	base	base	base	base	base d	base	base
A or C	or G	insertion	insertion	C OF F	C or T	A or G	insertion	insertion	insertion	A or T	A or G	A or G	deletion	G or F	deletion of	A or G	A or c
		of CA	of A				of GTTT	of A	Of A				of H	•	f GT		

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NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: pol-
                                                                                                                        NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: pol
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LOCATION: 99075..99121
OTHER INFORMATION: polymorphic
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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic
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NAME/KEY: allele
LOCATION: 160031
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OTHER INFORMATION:
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ
                 NAME/KEY: allele
LOCATION: 99094..99140
                                                                                                                                                                                                                                                  IOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ
                                                                                                                                                                                                                                                                             FEATURE:
NAME/KBY: allele
                                                                                                                                                                                                                                                                                                             THER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
GOCATION: 97130..97177
                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: polymorphic fragment
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 97099..97145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
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LOCATION: 93690..93736
OTHER INFORMATION: pol
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VAME/KEY: allele
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JOCATION: 88050..88096
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OCATION: 72771..72817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THER INFORMATION:
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                                                             polymorphic fragment
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                                                                                                                             5-130-257
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                                                             5-130-276 SEQ
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                                                                                                                             SEQ
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LOCATION: 108084...
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
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Query Match
Best Local Similarity
Watches 21; Conserve
                                                                                                           OTHER INFORMATION: polymorphic fragment
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 106918..106966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 103783..103828
                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 108127..108177
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: 106918..106966
TGAAAACTTGTGTAATTATGAAAT 28
                                                                                                                          108127..108177
                                                                                                                                                                                                                                                                                                                   108084..108130
                              Conservative
                                                                                                                                                                                                                                   .108130
: polymorphic fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphic fragment 5-133-375 SEQ
                                                                                                                                                                       polymorphic fragment
                                                                                                                                                                                                                                                                                                  polymorphic fragment
                                          61.9%;
                                             Score 19.2;
Pred. No. 1.
                              Mismatches
                                                                                                              5-135-198
                                                                                                                                                                            5-135-198
                                                                                                                                                                                                                                        5-135-155
                                                                                                                                                                                                                                                                                                    5-135-155 SEQ
                                        , μB 4;
(.1e+02;
                                                                                                              SEQ
                                                                                                                                                                          SEQ ID39
                                                                                                                                                                                                                                        SEQ
                                                         Length 162450;
                                                                                                              D9GI
                                                                                                                                                                                                                                        IDSS
                                                                                                                                                                                                                                                                                                    ID38
                                                                                                                                                                                                                                                                                                                                                                                                                               ID37
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ocal Samiarity 97:3; Pred, No. 1.18402; Indels 0; Gaps
s 21; Conservative 0; Mismatches 3; Indels 0; Gaps
s Totalacorrorogrammarchaer 28
14062 Totalacorrorogrammarchaer 14085

0

COMPUTER: IRM PC COMPATIBLE
OPERATING SUSTRIA: PC COMPACTO
SOFTWARE: PATENTIA Release #1.0, V
CURRENT APPLICATION NAMER: US/08/887,080
PLICATION INMER: US/08/887,080
PLICATION LABSIFICATION HAVE
CLASSIFICATION: 415
PRICE APPLICATION HAVE
PRICE APPLICATION HAVE
PRICE APPLICATION HAVE Patent No. 5965427
GENERAL INFORMATION: APELICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 36/615
REFERENCE/DOCKET NUMBER: 4600-011 ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: APPLICANT: Gregory Dolganov TELECOMMUNICATION NUMBER OF SEQUENCES: Palo Alto Application US/08687080 Dehlinger & Associates Cambridge Avenue, Suite INFORMATION Human RAD50 Gene and Methods of Use 175 US/08/687,080 Version 250 # Thereof

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RESULT 10
PCT-US96-07709-18
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                                                                                     PCT-US96-07709-18
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Best Local Similarity 81.5
22; Conservative
                       Matches
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                                                   Query Match
                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY JACENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,02
REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                TELECOMOUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-9223
TELEPAX: 800 ID NO: 18:
                                                                                                                                                   TYPE: nucleic ecid grannenness: single TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Pc compatible
COMPUTER: IBM Pc compatible
OPERATING SYSTEM: Pc-Cose/Ms-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
SOFTMARE: Patentin Release #1.0, Version #1.25
ElilkG Date: 3.3-4MA-1996
ElilkG Date: 3.3-4MA-1996
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                MOLECULE TYPE: CDNA
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                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                      Local
                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1700
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14855 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                       23;
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                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colorado
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                       Conservative
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                                                                                                    3..593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic
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                                    76.7%;
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                    0; Mismatches
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                    Score 18.8; DB 5;
Pred. No. 1.9e+02;
0; Mismatches 7;
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Pred. No. 1.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 14855;
                                                 Length 594;
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Best Local Similarity
Matches 23, Conserva
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                                                                                                                                                                                                                                                                RESULT 12
PCT-US96-07709-27
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                                                                                                                                                                                                                                 Sequence 27, Application PC/TUS9607709 GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                              ABPLICANT: Tripy, Cynthia A.
ABPLICANT: Missewski Macy
TITUE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITUE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
MAMBER OF SEQUENCES: 43
                  COMPUTER READABLE FORM:
                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 80203
MEDIUM TYPE: Floppy disk
                                 COUNTRY: U.S.A.
ZIP: 80203
                                                                                CITY: Denver
                                                                                               STREET:
                                                                                               ADDRESSEE: Sheridan Ross & McIntosh STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
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                                                                Colorado
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Gaps 0;

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TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                              NAME: CONNEIL INFORMATION:
NAME: CONNEIL GATY J:
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMPUTER READMALE FORM:
MEDIUM TYPER: Floopy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-COM/MS-POS
SOFTWARE: DatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US96/07709
APPLICATION NUMBER: PCT/US96/07709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tripp, Cynthia A
APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
583 AAAGTGACATCTTCTGTTATTATCAAATAT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AAAGTGACATCTTCTGTTATTATCAAATAT 41
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                                     1 ATAGTGAAAACTTGTGTAATTATGAAATTT 30
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                                                                                                                                                                                                                                                                                                     594 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1700 Lincoln St., Suite 3500
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tripp, Cynthia A.
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                                                                                                                                                                                                                                                     single
                                                                                                               60.6%;
76.7%;
                                                                                         Score 18.8; DB 5;
Pred. No. 1.9e+02;
0; Mismatches 7;
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                                                                                                                                     Length 594;
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RESULT 13
PCT-US96-07709-28/c
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TELEPHONE: (303) 863-0223
TERREMATION FOR SEQ ID NO: 27
SEQUENCE THARACTERISTICS:
SENGTH: (744 base pairs
TYPE: nuclaic acid
STRANDENESS: single
T-US96-07709-28
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ATTORNEY/AGENT INFORMATION:
NAME: CORMEL! AGENT J.
REGISTRATION NUMBER: 32,020
REFERRANCE/DOCKET NUMBER: 2618
TELECOMMUNICATION IMPORMATION:
                                                                                                                     TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              COMPUTER READMANDE POOM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITSM PC Compatible
COMPUTER: ITSM PC COMPATIBLE
SOFTWARE: PATCHIAN THE ALBERT #1.0, Version #1.25
CUEZERY APPLICATION DATA: THE ALGORITHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
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CURRENT APPLICATION DATA:
                                                                                                                                                                          ANTOSNEY/AGENT INFORMATION:
NAME: COMMAIL GENT J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tripp, Cynthia A. APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                       SEQUENCE CHARACTERISTICS:
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FILING DATE: 23-MAY-1996
                          STRANDEDNESS: SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Denver
                                                                                                                                          TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/:
FILING DATE: 23-MAY-1996
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1700 Lincoln St., Suite 3500
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.9e+02;
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COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: INM PC compatible
OPERATING SYSTEM: F0-D05/MS-D05
OPERATING SYSTEM: F0-D05/MS-D05
CUREEDY APPLICATION DATA:
PSPLICATION MUSICA: PCT/MS96/07709
PSPLICATION MUSICA: PCT/MS96/07709
PSPLICATION MUSICA: PCT/MS96/07709
PSPLICATION MUSICA: PCT/MS96/07709
PSPLICATION TOTAL TOTAL
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Best Local Similarity
                                                                                                                                                                                                                            Sequence 26, Application PC/TUS9607709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
STREET:
CITY: Denver
CITY: Colorado
""ATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HEIMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND FROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                           APPLICANT: Tripp, Cynthia A.
APPLICANT: WISNEWSKI, NACCY
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sheridan Ross & McIntosh
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAMB/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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76.7%;
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Pred. No. 1.9e+02;
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Pred. No. 1.8e+02;
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STREET: 1700 Lincoln St., Suite 3500

CITY: Denver

CTTY: Denver

STATE: COLORAD.

COUNTRY: U.S.A.

COMPTER: READABLE FORM:

MEDIUM TYPE: PLOPPY disk

COMPTER: LEEP Competible

COMPTER: MEDIUM NOBER: 25.00

FILING DATE: 20.40A-198

FILICATION NUMBER: 25.00-PCT

FILING DATE: 20.40A-198

FILING DATE: CONN

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nucleic search, using sw model

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Run on: December 18, 2003, 09:02:17 '; Search time 998.098 Seconds (without alignments)
103.495 Million cell updates/sec

Scoring table: Title: Perfect score: US-09-889-491-14 1 atagtgaaaacttgtgtaattatgaaatttt 31

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters:

4423956

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

12: Published Applications NA:* / Ggm2 6/bcodate // julipina / 1857 ptmcoves seq * / Ggm2 6/bcodate // julipina / 1857 ptmcoves seq * / Ggm2 6/bcodate // julipina / 1857 ptm seq * / Ggm2 6/bcodate // julipina / 1858 ptm seq * / Ggm2 6/bcodate // julipina / 1858 ptm seq * / Ggm2 6/bcodate // julipina / 1859 ptm seq * / Ggm2 6/bcodate // Julipina / 1859 ptm seq * / Ggm2 6/bcodate // Julipina / 1859 ptm seq * / Ggm2 6/bco

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0 0 0				α	Result
14 15	12	10 9 8	765	. u 2 P	No E
21.4 21.4 21.4	21.4	21.6 21.4	21.6	27.8 23 22.6	Score
69.0	69.0	69.0 69.0	69.7	89.7 74.2 72.9	Query
150384 150384 150384	2704 3747	13377 653	7737 7737 7737	7771 7771 134 7737	Length
199	15	113	1510	1111°	BG
US-09-795-668-1 US-09-795-686-1 US-09-946-807-1	US-10-106-698-1371 US-10-071-766-33	US-10-311-455-1436 US-10-027-632-213232 US-10-027-632-213232	US-09-764-847-2001 US-10-092-154-2001 US-10-073-961-453	US-10-311-455-1945 US-10-311-455-1946 US-09-878-574-8312 US-09-764-887-453	ID
Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli		Sequence 1436, Ap Sequence 213232, Sequence 213232,	Sequence 2001, Ap Sequence 2001, Ap Sequence 453, App	Sequence 1945, Ap Sequence 1946, Ap Sequence 8312, Ap	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24,	23	22	21	20	19	18	17	16
19.8	19.8	19.8	19.8	19.8	19.8	19.8	19.8	19.8	19.8	20	20	20	20	20	20	20.2	20.2	20.2	20.2	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.6	21	21
63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	63.9	64.5	64.5	64.5	64.5		64.5	65.2	65.2	65.2	65.2	65.8	65.8			65.8	65.8	65.8	66.5	67.7	67.7
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14	14	13	13	14	13	14	13	11	10	13	10	14	13	14	13	14	14	13	13	13	14	14	13	13	14	13	13	14	13
US-10-027-632-251930	US-10-027-632-251929	US-10-027-632-251930	US-10-027-632-251929	US-10-027-632-269992	US-10-027-632-269992	US-10-027-632-269993	US-10-027-632-269993	US-09-918-995-37378	US-09-983-965-2215	US-10-240-453-227	-09-764-864	US-10-027-632-149366	US-10-027-632-149366	US-10-027-632-206477	US-10-027-632-206477	US-10-027-632-102216	US-10-027-632-102215	US-10-027-632-102216	US-10-027-632-102215	US-10-311-455-1222	US-10-027-632-195310	US-10-027-632-195309	US-10-027-632-195310	US-10-027-632-195309	US-10-027-632-46536	US-10-027-632-46536	US-10-311-455-1559	US-10-027-632-76212	US-10-027-632-76212
Sequence 251930,	Sequence 251929,			Sequence 269992,			Sequence 269993,	Sequence 37378, A	Sequence 2215, Ap	Seguence 227, App		Sequence 149366,	Sequence 149366,	Sequence 206477,	Sequence 206477,	Sequence 102216,	Sequence 102215,			Sequence 1222, Ap		-	Sequence 195310,	Sequence 195309,			39		Sequence 76212, A

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ALIGNMENTS

RESULT 1 US-10-311-455-1945

Sequence 1945, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:

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LENGTH: 7771	SEQ ID NO 1945	NUMBER OF SEQ ID NOS: 2424	PRIOR FILING DATE: 2000-09-01	PRIOR APPLICATION NUMBER: DE 10043826.1	PRIOR FILING DATE: 2000-06-30	PRIOR APPLICATION NUMBER: DE 10032529.7	PRIOR FILING DATE: 2001-07-02	PRIOR APPLICATION NUMBER: PCT/SP01/07537	CURRENT FILING DATE: 2002-12-16	CURRENT APPLICATION NUMBER: US/10/311,455	FILE REFERENCE: 5013.1014	TITLE OF INVENTION: cytosine methylation	TITLE OF INVENTION: Diagnosis of Diseases Associated with the immune System by De	APPLICANT: BERLIN, Kurt	APPLICANT: PIEPENBROCK, Christian	APPLICANT: OLBK, Alexander	CHILDREN THE CHARLES THE COLUMN TO THE COLUM
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TYPE: DNA ORGANISM: Artificial Sequence

; FEATURE; ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-1945 (Homo sapiens)

문 Ś Query Match 89.7%; Best Local Similarity 93.5%; Matches 29; Conservative 4650 ATAGTGAAATTTGTATAATTATGAAATTTT 4680 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31 0 Score 27.8; Pred. No. 3 Mismatches DB 2 Indels Length 7771;

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RESULT 2

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US-09-764-887-453
US-09-764-887-453
Sequence 453, Application US/09764887
Patent No. US20020042096A1
JENERAL INFORMATION:
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; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: 701101005H1

US-09-878-574-8312
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US-10-311-455-1946
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                                                                                      RESULT 4
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CURRENT PAINE DATE: 200-112-16
PRIOR PAPPLICATION NUMBER: PCT/EPO1/07-57
PRIOR PAINE DATE: 200-107-02
PRIOR PAPPLICATION NUMBER: DE 1003259.7
PRIOR PRIOR PAPPLICATION NUMBER: DE 1003259.7
PRIOR PAPPLICATION NUMBER: DE 10043826.1
PRIOR PAPPLICATION NUMBER: DE 10043826.1
PRIOR PAPPLICATION NUMBER: DE 10043826.1
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SEQ ID NO 1946
LENGTH: 7771
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Best Local S
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Patent No. US20020110548A1
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Publication No. US20030143606A1
                                                                                                                                                                                                                                    Matches
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LA ROSSA, Thomas J.
APPLICANT: LA ROSSA, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OP INVENTION: No.lete Acid Molecules and Other Molecules Associated with
TITLE OP INVENTION: Plants
File Repearance: 80-21(1401)8 (Acids Fr.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLEK, Alexander
APPLICANT: PIEREBROKK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determine OF INVENTION: Cycosine methylation
FILE REFERENCE: 501.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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Pred. No.
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Pred. No. 1e+02;
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                                                                                      ; ORGANISM: Homo sapiens
US-10-092-154-2001
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                                                                                                                                           FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER: 07 ESQ 1D NOS: 2003
Frior Application removed - See File Wrapper or Falm
SOFTWARE: Patentin Ver. 2.0
LEMONTH: 7130
LEMONTH: 7130
   Query Match 69.7%;
Best Local Similarity 85.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2001, Application US/10092154 Publication No. US20030054375A1
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LENGTH: 7737
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Best Local :
                                                                                                                                 TYPE: DNA
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Pred. No. 4.4e+02;

Length 7737;

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Mismatches

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-453
                                                                                                                    ; ORGANISM: Homo sapiens
US-09-764-847-2001
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SEQ ID NO 453
LENGTH: 7737
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2001, Application US/09764847 Patent No. US20020132767A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID-NOS: 658
                                                                                                                                                                                                                Prior application data removed - consult PALM or file wrapper NUMERE OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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mes 24; Conserv
                                                            Local Similarity
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4 GIGARACTIGIGIATIATGRAATITT 31
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                                         Conservative
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85.7%;
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Pred. No. 4.4e+02;
                                                            Score 21.6; DB 10;
Pred. No. 4.4e+02;
                                         Mismatches
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RESULT 7
US-10-073-961-453
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TITLE DE INTENTION BALSEC ACIDE, PROTESIAS, AN
TITLE DE INTENTION PALISC.
CURRENT PELLONION MUNERE: US/10/073,961
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PRICE PELLON DATE: 2002-03-05
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PRICE PELLON DATE: 2002-03-05
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PRICE PELLONION MOMBER: 05/180,068
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Publication No. US20
GENERAL INFORMATION:
                                              NE FILING DATE: 2000-09-29
NE PELICONTION UNDUBER: 60/224,519
NE PILING DATE: 2000-08-14
NE PELICANTION UNUBER: 60/220,964
NE FILING DATE: 2000-09-26
NE PELICANTION UNUBERS: 60/241,809
NE PELICANTION UNUBERS: 60/241,809
NE PELICANTION UNUBERS: 60/249,299
NE PELICANTION UNUBERS: 60/249,299
                                                                                                                                                                                                                                              EX APPLICATION NUMBER: 60/234,274
EX PILLING DATE: 2000-09-21
EX APPLICATION NUMBER: 60/234,223
EX PILLING DATE: 2000-09-21
EX APPLICATION NUMBER: 60/224,518
EX APPLICATION NUMBER: 60/224,518
EX APPLICATION NUMBER: 60/236,369
EX APPLICATION NUMBER: 60/236,369
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FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/217,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/217,487
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/214,886 FILING DATE: 2000-06-28
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FILLING DATE: 2000-07-07
APPLICATION NUMBER: 60/225,267
FILLING DATE: 2000-08-14
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APPLICATION NUMBER: 60/226,868
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PLICATION NUMBER: 60/236,327
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5. US20030077602A1
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APPLICATION NUMBER: 60/225,266

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RESULT 8
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Best Local
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,207
                                                                                                                                                                                                                                                                                  FILING DATE: 2000-10-20
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APPLICATION NUMBER: 60/241,221
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/241,786
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FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,397
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FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/249,215
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APPLICATION NUMBER: 60/249,213
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APPLICATION NUMBER: 60/231,243
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FILING DATE: 2000-09-14
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FILING DATE: 2000-09-08
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                                                                 GIGARACATIGIGIAATTACTAAATTT 4112
                                                                                          GTGAAAACTTGTGTAATTATGAAATTTT 31
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85.7%;
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                                                                                                                                  Score 21.6; DB 15;
Pred. No. 4.4e+02;
0; Mismatches 4;
                                                                                                                                                                      Length 7737;
                                                                                                                                       Indels
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PRIOR ENTICATION NUMBER: DE 10022829.7

PRIOR FILIAND BATE: 2000-06-30

PRIOR REPLICATION NUMBER: DE 10043826.1

PRIOR PELICATION NUMBER: DE 10043826.1

PRIOR PELICATION BATE: 2000-09-01

NUMBER: OF SEQ ID NO.5: 2424

SEQ ID NO.1456

LENGTH: 1.3377

TIPB: DNN
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; ORGANISM: Human
US-10-027-632-213232
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                                                                                                                                                                                                         PRIOR MPELCANTION NUMBER: US 60/193,483
PRIOR FILINA NATE: 2000-03-29
PRIOR REPLICANTION NUMBER: US 60/185,218
PRIOR REPLICANTION NUMBER: US 60/185,288
PRIOR REPLICANTION NUMBER: US 60/187,383
PRIOR PELICANTION NUMBER: US 60/187,383
PRIOR PELICANTION NUMBER: US 60/186,388
PRIOR PELICANTION NUMBER: US 60/186,388
PRIOR PELICANTION NUMBER: US 60/186,388
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Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 213232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PIEPENBROCK, Christian
APPLICANT: BEELIN, Murt
TITILE OF INVENTION: Diagnosis of Diseases
TITILE OF INVENTION: Optosine methylation
FILE REPERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: dentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymoxphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                        PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: chemically treated genomic DNA
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                                                    TYPE: DNA
                                                                          ENGIH: 653
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Pred. No. 4.8e+02;
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Query Match 69. Best Local Similarity 80. Matches 25; Conservative

80.6%;

Score 21.4; DB 13; Pred. No. 3.4e+02; 0; Mismatches 6;

Length 653;

0;

Gaps

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US-10-027-632-213232
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US-10-027-632-213232
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US-10-106-698-1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 213232
                                                                                                                                                                   SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 1371
LENGTH: 2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1371, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                PILE REPRENCE: PAOSEN
GURERNY APPLICATION NUMBER: US/10/106,698
CURERNY FILING DATE: 2002-03-27
CURRENY FILING DATE: 2002-03-27
REIOR APPLICATION NUMBER: PCT/US002/6554
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PILING DATE: 1939-09-29
PRIOR PILING DATE: 1939-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/163,280 PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polymucleotides and Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-08-09
                          NAME/KEY: misc_feature
LOCATION: (1438)..(1438)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 486 ATAGTGACATCTTGTGGAATCATCTAATTTT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
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Pred. No. 3.4e+02;
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                                  OF.
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NUMBER OF SEQ ID NOS: 1531 SOFTWARE: FastSEQ for Windows Version 4.0

IOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c OTHER INFORMATION: r=g or a NAME/KEY: misc_feature LOCATION: (1)...(1531)

NAME/KEY: misc_feature

INFORMATION: m=a or c

NAME/KEY: misc_feature

FEATURE: TYPE: DNA ORGANISM: Homo sapiens

ENGTH: 1503841

PRIOR FILING DATE: 2000-02-28

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RESULT 12
US-10-071-766-33
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US-09-795-668-1/c
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 25; Conserv
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SOFTWARE: PERL Program
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/10071766
publication No. US20020192678A1
GENERAL INFORMATION
APPLICANT: Huel-Mei Chen
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Best Local Similarity
                                                                        GENERAL IMPORMATION:
APPLICANT: Stefanson, Hreinn
APPLICANT: Stefanthorsdottir, Valgerdur
APPLICANT: Galcher, Jeffrey R.
APPLICANT: Galcher, HUMAN SCHIZOPHRENIA GENE
                                                                                                                                                                  Sequence 1, Application US/09795668
Patent No. US20020045577A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 09/515,716
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LOCATION: 3223-3355
OTHER INFORMATION: a,
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OTHER INFORMATION: Incyte ID No. US20020192678A1 1330122.9
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ORGANISM: Homo sapiens
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Pred. No. 4.4e+02;
0; Mismatches 6;
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                              4.6e+02;
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US-09-795-668-1
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Best Local Similarity
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LENGTH: 1503841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
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SOPTWAPE: PARTY SOTTWAPE: PARTY SOPTWAPE: PARTY SOTTWAPE: PARTY SOTTWAPE: PARTY SOTTWAPE: PARTY SOT
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APPLICANT: Stefinthorsdottir, Valgerdur
APPLICANT: Golicher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g
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LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g
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LOCATION: (1)...(1531)
OTHER INFORMATION: wea or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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OTHER INFORMATION: 8=9
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NAME/KEY: misc feature
LOCATION: (1) ... (1531)
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LOCATION: (1)...(1531)
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OTHER INFORMATION: s=g
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NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc feature
LOCATION: (1) - (151)
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LOCATION: (1)...(1531)
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Pred. No. 9.5e+02;
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Best Local Similarity
Wearches 25; Conserve
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US-09-946-807-1/c
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Patent No. US20020165144A1
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LOCATION: (1):...(1531)
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CURRENT APPLICATION WINERER: US/09/946,807
CURRENT FILLAG DATE: 2001-09-05
PRICH APPLICATION NUMBER: US/09/795,668
PRICH FILLAG DATE: 2001-02-28
FRICH FILLAG DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/515,716
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OM nucleic - nucleic search, using sw model
                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:

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22781392 seqs, 12152238056 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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688. GSS 16-APR-2003

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Acides segypti (yellow fever mosquito)

acide yellow fever mosquito)

acide yellow ference, Arthropods, Hexapods, Insecta, Pterypota,

Reoptera; Bandopterypota; Daptera; Nematocera; Culicoides; Aedes.

(Chasse 1 to 181)

Lottus B., Shetty, J., Severson, D., Brown, S. and Knudson, D.

and sequencing of Aedes segypti BACs

Impublished

REFERENCE COMMENT AUTHORS TITLE

Other_GSSs; CSU-K33r.34G16.SP6 Contact: Brendan Loftus Department of Bukaryotic Genomics

9712 Medical Center Drive, Rockville, MD 20850, USA Tel. 301-393-3543 Tex. 301-393-050 Bmail: entackign org Library was provided by Susan Brown and Dennis Knudson at Colorado Scate University. Seq primer: TY

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RESULT 3
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CSU-K331.34G16.SP6 CSU-K331 Aedes aegypti
CSU-K331.34G16, genomic survey service
CCOSSE70
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Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loftus, B., Shetty, J., Severson, D., B
End sequencing of Aedes aegypti BACs
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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CC088678.1 GI:29944112
                                                                                                                                                                                                                                                                                                                                                                   Email: enta@tigr.org
Library was provided by Susan
State University.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insu
Neoptera; Endopterygota; Diptera; Nematocera;
1 (bases 1 to 242)
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                                                                                                                                                                                                                                                                                                                                                                                                              ax: 301-838-0208
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                                                                                                                                                                                                                   Aedes aegypti (yellow fever mosquito)
Aedes aegypti
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                    Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
                                                                                           Department of Eukaryotic Genomics
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79.4%;

0 Score Pred.

Mismatches

Indels Length

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24.6; DB 29 No. 2.1e+02;

29;

537;

GI:29915019

linear GSS 16-APR-2003 genomic clone

Drive, Š.

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Susan

Brown

and Dennis Knudson at Colorado

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CC11562
NDL.35011.77 Notre Dame Liverpool Aedes aegypti
NDL.35011, genomic survey sequence.
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Library was provided by David
Seq primer: T7
Class: BAC ends.
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1. Chases 1 to 537), Knudson, D. and Sever BAC end sequencing of Aedes acgypti
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Tel: 301-838-3543
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                                                                                                                                                                                                                                                                                                                                                                                                                         ax: 301-838-0208
/cognition="Andes acypt!"
/mol_type="generation DNN"
/przain="Liverpool"
/db.yrcg="reaconto DNN"
/db.yrcg="reaconto DNN"
/db.yrcg="reaconto DNN"
/dlone="MOCTON: 1953AG1; Site_1. Hind III; The library was prepared from whole body bisence of newly hacched Li larvae by bavid severeon at the University of Notre Dame and Hoogbin Enange
by David Severeon at the University of Notre Dame and Hoogbin Enange

by David Severeon at the University of Notre Dame and Sor c 161 g 162 t
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574 ATAGTGAAAATTGTGAAATTATGGTATTTT 604
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                                                                                                                                                                                                                                                                                                                                                                                                                       Other GSSs: NDL.60K24.SP6
Contact: Brendan Loftus
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Seq primer: T7
Class: BAC ends.
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Loctus, B., Shetty, J., Knudson, D. and Severson, BAC end sequencing of Aedes aegypti
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Aedes aegypti
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Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic
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/mol_type="genomic DNA*
/scrain="Rexville"
/bb_xref="taxon:7159"
/clone="CSU-X331.5020"
/clone="CSU-X331.5020"
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/clone_ibb="CSU-X331.5020"
/clone_ibb="CSU-X331.5020"
/note="Yestor: pBeloBAC11; 8
                                                                                                                      Hongbin
a 106
                                                                                                                                              /clone lib="Notre Dame Liverpool"
/note="Mector: pXCBACI; Site 1: Hind III; The library was
pregared from whole body tissue of newly hatched Li larva
by David Severson at the University of Notre Dame and
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                                                                                                                                                                                                                  /organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
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source

organism="Tetraodon nigroviridis' /db_xref="taxon:99883" mol_type="genomic DNA"

AUTHORS

Matches Query Macch

89

1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31

ATTGTGAAAGGTTGAGTAATTATGAATTTTT 59

Agolisias Agolisias (1984) by DNA linear GSS 05-Max HS 2208_B2_E05_T7C CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=2208 Col=10 Row=J, genomic survey

GSS 05-MAY-1999

AQ515182 AQ515182.1

GI:474744(

Local

Similarity

74.2%; 83.9%; 0;

Score 23; DB 29; Pred. No. 7.5e+02;

Length 524;

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Mismatches

Conservative

192

/dixes con-/clone lib-"G" /clone lib-"G" /note-"Genoscope sequence ID : COAGZOSBAQNIFI-end : /note-"Genoscope 3 172 t 6 others

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Bernot,A., Fishers,C., Mincher,F., Brotties,F., Queiter,F.,
Betinate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DRN sequence
Nat. (Semet. 25 (2), 233-238 (2000)
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Tetraodon nigroviridis
Tetraodon nigroviridis
biriect Submission

Submitted (11.24R-2000) Genoscope - Centre National de Sequencage :
Bu 191 91006 ENRY cedex - PRANCE (8-mail : seqrefégenoscope cms.fr

This sequence is a stinjle read and was generated as part of a large
scale clome-end sequencing project of the Terracodom ingroviridis
genome. For more information, please take a look at
http://www.genoscope.cms.fr/Tetracodom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosest Crollius, H., Jaillon, O., Desilva, C., Ozonf-Costas, C., Fizames, C., Carollon, C., Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostoni;
Actinopterygil; Neopterygil; Paleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygil; Percomorpha; Tetraodontiformss;
Tetraodontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31
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Bax11. yallacebu washington edu
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Class: BAX2. ends.
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (hoasea | to 543)

Mahairas, G.G., Wallace, J.C., Smith, K., Swarzsell, S., Holman, T.,

Mahairas, G.G., Wallace, J.C., Smith, K., Swarzsell, S., Holman, T.,

Melier, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. at

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. at
                                                                                                                    Dumi, D., Aeyagi, A., Bather, M., Beacorn, T., Duval, B., Hamil, C., Italam, H., Longorre, S., Nahmoud, M., Meenen, S., Podersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Mright, D., Meise, R., Stokes, R., Tingey, A., von Niederhausern, A., House, whole genome scaffolding with paired end reads from 10kb fromes.
                      University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                  GSS
                                                                                                                                                                                                                                                                                                                                                                                         AZ997354 Jinear GSS 27-ARR-200
2M0283B21R Mouse 10kb plasmid UNGCZM library Mus musculus genomic
clone UUGCZM0283B21 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                Contact: Robert B.
                                                                                Unpublished
                                                                                                       plasmid inserts
                                                                                                                                                                                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostoni;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mas
L (bases 1 to 595)
                                                                                                                                                                                                                                                                                        Mus musculus
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308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                           musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 543.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CIT Approved Human Genomic Sperm
/notes="Organ: sperm; Vector: pBeloBAC11; BAC
B-Colis=10108" 99 g 160 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2208 Col=10 Row=J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.2%;
83.9%;
                                                             Weiss
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Pred. No.
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   20 S.
2030 B.,
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   SLC,
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ORGANISM
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AZ868713
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KEYWORDS
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                                             COMMENT
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                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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Plate: 0283 row: B column: 21
Seg primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
University of Utah
University of Utah
                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
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                                             Contact: Robert B.
                                                                                plasmid inserts
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                                                                Unpublished
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Pred. No. 7.
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High quality sequence stop: 595.
Location/Qualifiers

/lab hose-"B. coli strain XL10-Gold, "I-resistant, F-"
/clome Lib="Mouse 10kb plasmid UUGCZM library"
/bote="Wector: PMP42rv; Bruified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson /db_xref="taxon:10090" /clone="UUGC2M0283B21" mol_type="genomic strain="C57BL/6J" organism="Mus musculus" |mol_type="genomic nva"

habboutcopy Mouse DNA Recourse

(http://www.jux.cog/resources/documents/domarces/). The DNA
was inducedynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotick kinase, Andpto orlogomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored BNA was purified and size-sealected for a 9.5 to
10.5 Mr range using preparative agazose gel
electrophoresis. Vector DNA was perpared from a derivative
of pNn22 (gil4732114 [gh] AP129072.1), a copy-number
inducible decrivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored use DNA, and transformed liteo was annealed to
adaptored overcomplement allocal Multonia decreases of complementary to the sheared adaptored consecutive complement and provided the consecutive complement and provided the complement of the sheared adaptored mouse DNA was annealed to
adaptored overcomplement and provided the consecutive complement of the consecutive c

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Length 595

0 Gaps

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1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31 Mismatches).6e+02; 5;

clone UUGC2M0180I02 R, genomic survey sequence. 2M0180102R Mouse 10kb plasmid TUGCIM library Mus musculus genomic dq 919 DNA GSS 21-FEB-2001

Bukaryota, Wetazos, Chordeta, Cremiata, Vertebrutu, Buteleostoni, Mammalia, Butheria, Rodentia, Schuropathi, Muridee, Murinee Mus.

1 (based 1 to 616)

Dunn, D., Aoygal, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Italian, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Railly M., Xosa, M., Roes, R., Stokes, R., Tingey, A., von Miederhausern, A., and Wright, D., Weise, S., Stokes, R., Tingey, A., von Miederhausern, A., Money, Money, Moley Growne Scaffolding with paired end reads from 10kb Genome Center

FEATURES

source

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Query Match
Best Local Similarity
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84112, US
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Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: I column: 02
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Canista; Vertebrata; Buteleostomi, 
Nammalia; Butheria; Primates; Catarthin; Hominidae; Homo.
1C Chases I to 668)
NCI CGAP http://www.nobi.nlm.nih.gov/ncicgap.
NRI CAGAP http://www.nobi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ002494 668 bp mRNA linear EST 26-MAR-2002
UI.H-EII-ayw-d-03-0-UI.s1 NCI_CGAP_EII Homo sagiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ002494
BQ002494.1 GI:19727394
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE:5844434 3', mRNA sequence.
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAGTGAACACTTGTGGAATCATCAGATTTT 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.jax.org/resources/documents/dnares/. The DNA was bydrocynamically sheared by repeated passge through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 1% DNA polymerase and 7% polymuclaotide kinase. Adaptor oligonuclaotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 hb range using preparative agarose gel. 10.5 hb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of purity (4):473214 [9]:1872071.3] a copy-rumber ligated inducible derivative of planning R. The vector was and with sady brong complementary to the house of the planning and the property of the planning of the pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purified, The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into Chemically-competent 8. coli XLO-Gold (Stratagene) cells and selected for amplicillar seeistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Jab host="B. Coli strain XIAO-Gold, Th-resistant, F
/clome lib="Mouse 100b plasmid UUGCHM library"
/note="Vector: PMD42IV; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
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AUTHORS
TITLE
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                                                                        FEATURES
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                                                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, Tel: 301-838-3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aedes aegypti (yellow fever mosquito)
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ORIGIN

Matches

BASE COUNT

EQ002494

용

558

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DNA Sequencing by: Dr. M. Beato Soares, University of Load Clone Distribution: Clone distribution information can be through the I,M.A.G.E. Consortium/Likhu at: http://image.lln
Seq primer: M13 FORWARD
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Location/Qualifiers

/lab_bote* mpitos (tite pechnologies)*

/alone lib=writ Cabe Eil*
/alone lib=writ Cabe Eil*
/abore="Organ: Left pēlvis; Vector: pv773-pac (Pharmacia)
/note="Organ: Left pēlvis; Vector: pv773-pac (Pharmacia)
/note="Organ: Left pēlvis; Vector: pv773-pac (Pharmacia)
/note="Organ: Left pector products of the products of the products of the pv674 pac (Pharmacia)
/note constructed according to Bonaldo, Lennon and Soares,
/eanome Research, 6:791-905, 1996. Pirst strand CBNA
/note pv771-80bb e stranded CDNA was ligated to an Egod i
/note I site, Double stranded CDNA was ligated to an Egod i
/note pv771-80bc effort. The pv674-80bc lies(i ob pv18me
/note pv774-80bc effort. The pv674-80bc lies(i ob pv18me
/note pv774-80bc effort. The pv674-80bc lies(i ob pv18me
/note pv774-80bc effort. The pv674-80bc lies(i ob pv18me) TAG_SEQ=ACACTTGCAC TAG_LIB=UI-H-EI1 the synthesis of first-strand cDNA contains a library sequence that is located between the Not I site and the /organism="Homo sapiens" (dr)18 tail. The sequence tag for this library is dev_stage="Adult" 'tissue_type="Chondrosarcoma" clone="IMAGE:5844434" mol_type="mRNA" db_xref="taxon:9606" TISSUE=chondrosarcoma Consortium/Link at: http://image.llnl.gov 1 others I site and the found

Local Similarity 1 ATAGTGAAAACTTGTGTAATTATGAAATTTT 31 ACAGTGAACACTTTTATAATTATGAATTTTT 180 Conservative 74.2%; 0; Score 23; DB 12; Pred. No. 7.8e+02 Mismatches Length 668; Indels 0

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223 t

NDL.51F5.T7 Notre Dame Liverpool Aedes NDL.51F5, genomic survey sequence. CC120192 .1 GI:29989247 aegypti genomic clone linear GSS 16-APR-2003

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes. 1 (bases 1 to 814) Loftus, B., Shetty, J., Knudson, D. and Severson, D. BAC end sequencing of Aedes aegypti Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Culicoidea; Aede

Unpublished

Department of Eukaryotic Genomics Contact: Brendan Loftus MD 20850,

Email: enta@tigr.org Library was provided by David Severson Seq primer: T7 Class: BAC ends. Fax: 301-838-0208

/organism="Aedes aegypti" Location/Qualifiers

COMMENT

REFERENCE

STIIL AUTHORS ORGANISM KEYWORDS VERSION ACCESSION DEFINITION RESULT 10

BASE CO

COUNT

밁 Ś

172

Matches

Local

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Wylie,
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vector to vector length is 233
vector respective from glibco.
Seq primer: 40RP from glibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available through: ResGen, Invitro South Memorial Parkway Huntsville, AL 35801 For call: (800)-533-4363 or contact: cou@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Umpublished
Umpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Mashington Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,R., Ritter,E., Kohn,S., S., R., Waterston,R. and Wils
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; rosió; eurosids I; Fabales; Fabaceae; Puphlionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max (soybean)
Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shomakor, R., Kein, F., Vodkin, L., Erpelding, J., Corpell, V., Khanni, A., Bolla, B., Marra, M., Hillier, L., Kuoba, T., Martin, J., Beck, C. Wyle, T., Underwood, K., Stepton, M., Theising, B., Allen, M., Bower, Y., Erson, B., Swaller, T., Gibbons, M., Rape, D., Harvey, M., Schmit, E., Mitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Matcreton, E., and Milson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Notice Dame_Liverpool"
//clone_lib="Notice Dame_Liverpool"
//pote="Vector: packack; Site_l: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Saverson at the University of Notre Dame and Hongbin Enang"
210 c 149 g 219 t
                                                                                                                                                                    /tissue_type="Germinating
/lab_host="DH10B"
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                                                                                                                                                                                                                 Clone="SOYBEAN CLONE ID:
                                                                                                                                                                                                                                                                   'mol_type="mRNA"
                                                                                                                                                                                                                                                                                                organism="Glycine max"
                                                                                                                                                                                                                                              xref="taxon:3847"
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Pred. No.
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shoot, 24 hour
                                                                                                                                                                                     shoot,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further information
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REFERENCE

AUTHORS

KEYWORDS VERSION ACCESSION DEFINITION TOCOS. BM885747 RESULT 12

ORGANISM

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poly(df) sequence with a MhoI restriction site. EcoRI adapters were lighted to the blunt-redded cDNA fragments followed by MhoI digestion. The CDNA fragments were directionally cloned into the EcoRI-MOI restriction site of the pBluescript vector. The lighted cDNA fragments were transformed into BHIOB horse cells (Suboc BNA). This
library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."
21 c 33 g 72 t
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Query Match Best Local 25; Similarity Conservative 72.9%; 86.2%; 0, Score 22.6; DB 1: Pred. No. 8.7e+02 Mismatches 12; Length 0 Gaps 0

Matches 74 N TAGTGAAAACTTGTGTAATTATGAAATTT 30 TAGTGAAAACTTGTGTAAGTTTGAATGTT 102

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ORIGIN

BASE COUNT

106

VERSION KEYWORDS RESULT 13 BE330627 LOCUS ORGANISM ACCESSION DEFINITION Glycine max Glycine max BE330627, yi Gm-q1040 Glychae max CHUR clone GENOVE SYSTEMS CLONE ID: 608207, yi Gm-q1040 Glychae max CHUR clone GENOVE SYSTEMS CLONE ID: 608-01040-2149 5, similar to TR:Q43015 Q43015 ALCOHOL BE330627.1 DEHYDROGENASE-1CN ;, mRNA sequence. GI:9204403 (soybean)

REFERENCE Bukaryota, 'Wirddplantae, Streptophyta, Embryophyta, Trachaophyta, Spermatophyta, Megnoliophyta, emidoctyledons, core endicots; rosids ; eurosids I; Pabales, Fabaceae, Papilionoideae, Phaseoleae; Glycine. (bases 1 to 434)

AUTHORS Shoemaker, R., Kedim, P., Vodkin, L., Erpelding, J., Coryell, V., Khaman, A., Bolla, B., Marran, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylae, T., Underwood, K., Septcea, M., Theising, B., Allen, M., Bowers, Y., Pezron, B., Sealier, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., HCamman, R., Maccarton, R., and Wilson, R.

JOURNAL Unpublished Public Soybean EST Project

COMMENT

Contact: Shoemaker R/Public Soybean EST Project

FEATURES Bource

FEATURES

source

COMMENT

JOURNAL,

/mol_type="mRNA" /db_xref="taxon:1847" /clone="GENOME SYSTEMS CLONE ID: Gm-c1040-2149" organism="Glycine max"

(clone lib-wom-clo4d)"
(folore lib-wom-clo4d)"
(folore "Wottor: prTTIPRo (Pharmacka); Site 1: EcoRI;
(folore "Wottor: prTTIPRo (DBN library was constructed from mENN isolated from hypocotyl and plumule itssues of seeds germinated for three days of the cultivar Williams 82.

Seminated for three days of the cultivar Williams 82.

Seminated for three days of the cultivar Williams 82.

Seminated for three days of the cultivar with most user restriction consisting of a poly(df) sequence with a Not! restriction site. EcoRI daphters were lighted to the blunt-ended construction of the cultivar was seminated to the cultivar was seminated tissue_type="Hypocotyl and Plumule, germinating seeds" | Jab_host="DH10B"

synthesized from mRNA using a primer consisting

of a

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Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2110
South Memorial Parkway Huntsville, AL 35801 For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Poreset Park Barkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A., Bolla, B., Marra, M., Hillier, J., Monba, T., Martin, J., Beck, C., Wylis, T., Underwood, K., Steptoe, M., Theisting, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibons, M., Pape, D., Harvey, M., Schutk, X., Ritter, E., Nohn, S., Shin, T., Jackson, Y., Cardenas, M., McCam, R., Matcerton, E., and Wilson, R.
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Shoemaker, R., Keim, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Trachoophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids i; Fabales; Fabaceae; Papiliomoideae; Phaseoleae;
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BQ611630.1 GI:21601299
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Gm-c1087-5369 5' similar to TR:Q43015 Q43015 ALCOHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.resgen.com
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEHYDROGENASE-1CN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector to vector length is 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                        primer: -40RP from Gibco
h quality sequence stop: 454
Location/Qualifiers
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                                                                 (clone lib="Gm-cl087" (clone lib="Gm-cl087" (riche lib="Gm-cl087" (riche lib="Voctor: pBluescript II SK+, Site_1: EcoRI; Site_2: MooI; The GNUM was prepared uping polystrate EREMA SYSTEM from FROWEGA. The CDUM was synthesized from EREM using the Stite Complementary DNA was synthesized from EREM using primary consisting of a poly (dr) sequence with a MooI primary consisting of a poly (dr) sequence with a MooI
                                                                                                                                                                                                                      /clone="SOYBEAN CLONE ID: Gm-c1087-5369"
/tissue_type="Roots"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                           /organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.9%;
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Pred. No. 9.8e
0; Mismatches
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Brassica oleracea

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermscophyta, Magnoliophyta, endicotyledons, core endicots, rosids

entroids II, Brassicales, Brassicaeae, Brassica.

(Cases 1 to 565)

Town, C.D., Van Aben, S., Utterback, F., Xoo, H. and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whole genome shotgun sequencing of Brassica oleracea Unpublished Other_GSSs: BOMSU91TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smail: cdtown@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="BO_2_3_KB"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1, Site_1: BstXI, 2-3 kb
genomic_DNA inserted into pHOS1 using BstXI
a 110 c 80 g 201 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Rockville,

죵

20850, Tom Osborn

provided by

REFERENCE AUTHORS

Glycine.

SOURCE VERSION DEFINITION

ORGANISM

Glycine max

KEYWORDS ACCESSION

COMMENT

JOURNAL.

PEATURES

source

2003,

11:35:09

536

0

Mismatches

4

0

Gaps

0,

Score 22.6; Pred. No. 16

1e+03; DB 29;

Length

565;

RESULT 14 BQ611630 LOCUS

B 8

331 25;

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Mismatches

bp DNA

genomic clone

BOMSU91 GSS 16-DEC-2002

DNA

linear

Score 22.6; DB Pred. No. 1e+03;

13;

Length

553;

0, Gaps

0

Query Match

Conservative

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OM nucleic - nucleic search, using sw model
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December 18, 2003, 09:02:17; Search time 196.721 Seconds
(Withburth time 196.721 Seconds
411.664 Million cell updates/sec

Title: Perfect score: Sequence: US-09-889-491-13 30

1 atatagaagcccaagaaaaatcagctgacc 30

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS1/jcgdata/jenesed/jenesedn-emb1/NA1984.DAT:*
(SIDS1/jcgdata/jenesed/jenesedn-emb1/NA1985.DAT:*
(SIDS1/jcgdata/jenesed/jenesedn-emb1/NA1985.DAT:*
(SIDS1/jcgdata/jenesed/jenesedn-emb1/NA1987.DAT:*

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Pred. No. is the number of results predicted by chance to have a soore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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20	20.4	20.4	22.2	22.2	22.2	30	30	Score
66.7	68.0	68.0	74.0	74.0	74.0	100.0	100.0	Query
3610	6816	2528	17087	17087	2577	2421	30	Query Match Length DB
24	22	24	24	20	23	21	21	뛿
ABN95909	AAS46688	ABA05477	ABS98779	AAX12984	AAS53160	AAA61936	AAA74857	Ħ
Gene #2407 used to	Tumour suppressor	Human RNA gyrase 1	Enterococcus faeca	Enterococcus faeca	Enterococcus faeca	Human bone sialopr	Human bone sialopr	Description

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19	19	19	19	19	19	19	19	19	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.6	19.6	19.6	19.6	19.6	19.6	19.6	20	20	20	20
63.3	63.3	63.3	63.3	63.3			63.3		64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	65.3	65.3	65.3	65.3	65.3	65.3	65,3	66.7	66.7	66.7	66.7
716	613	483	483	483	483	483	483	483	20561	20561	3466	3466	2478	2169	1695	6854	6854	6854	2507	902	623	623	623	460	406	52354	1786	1103	817	547	539	508	2365589	5088	3610	3610
24	18	24	23	22	22	22	22	22	24	20	20	16	13	23	24	20	19	16	22	24	22	22	22	22	23	24	22	22	22	22	22	22	24	23	24	24
ABQ68688	AAT93779	ABS07046	ABS31975	AAI38122	AAK32269	AAK06580	ABA27545	ABA58469	ABS99024	AAX13229	AAV71918	AAQ99883	AAQ27388	AAS53062	ABZ31862	AAV71898	AAV21508	AAQ99852	AAH29717	ABN74646	AAK85426	AAK85425	AAK85424	AAK63650	AAS58703	AAD35032	AAH16754	AAH72866	AAH08594	AAH71172	AAH69370	AAH72236	ABA90521	ABL17238	ABL68604	ABL62384
Listeria monocytog	Oryza sativa patho	Human genome-deriv	Human liver single	Probe #6808 used t	Human bone marrow	Human brain expres		-		cerococcus	S. cerevisiae KAR3	KAR3 coding sequen	Protein disulphide	Enterococcus faeca	Candida albicans e	S. cerevisiae TIH2	S.cerevisiae TIH2	Yeast TIH2 gene.		Bovine embryonic g	Human immune/haema	Human immune/haema	Human immune/haema	Human immune/haema	cDNA #1379 encodin	Human transporter	cDNA seg		Human cDNA clone (Human cervical can	Human cervical can	Human cervical can	Genomic sequence o	Drosophila melanog	Kidney cancer rela	Colon adenocarcino

ALIGNMENTS

RESULT 1 AAA74857 ID AAA

AAA74857 standard; DNA; 30 BP

AAA74857;

17-JAN-2001 (first entry)

Human bone sialoprotein gene promoter BSP-A1496G polymorphic site.

Human; bone sialoprotein; BSP; bone mineral density; atherosclerosis; osteoporosis; promoter; ds.

艾莫莫艾 Homo sapiens.

variation

Location/Qualifiers
replace(16,G)
/*tag= a
/*note= "BSP-A1496G polymorphism"

WO200042216-A2.

20-JUL-2000.

17-JAN-2000; 2000WO-EP00319.

18-JAN-1999; 28-MAY-1999;

99GB-0001037. 99GB-0012585.

(OSTE-) OSTEOMETER BIOTECH AS

Kugk

WPI; 2000-476070/41

Assessing predisposition to a calcification condition status such as osteoporosis and atherosclerosis, comprising determining the genotyp of the promoter of the bone sidioprotein, matrix gla protein,

genotype

or osteoprotegerin gene -

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X3XEXEXEXEXEXX8XEXEXEXEXEXEXEXEX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bone sialopoteśni promoter; BBP; human; tismae-specific promoter; brytanystical component of the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence at polymorphisms in a number of genes controlling bone minaral density. These genes include sequences encoding the bone staloprocesh, the matrix gla protein (MgP), osteopontin (OPM) and cotoportegarchin (othick) actor (OPG/OCTF). G at this position is associated with a higher peak bone mass. Along with the other polymorphic sites, this variable sequence can be used to predict an individual's predisposition to osteoporosis and atheroscierosis, thus enabling entire treatment and preventive measures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence shows the polymorphic sit was position 149% of the month one slatoprotes (BSP) gene promoter. It was used in the of the invention, which involve the determination of the promoter.
                                                                                 Novel therapeutic agent for prevention and treatment of calcified tumors and proliferative disorders such as osteosarcoma, multiple mysloma and breast cancer, comprises bone sialoprobein promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bone sialoprotein (BSP) promoter (-2184-+237).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA61936 standard; DNA; 2421 BP
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                           Claim 5; Fig 8A-B; 79pp; English
                                                                                                                                                                                                   WPI; 2000-442489/38.
                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1999;
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Pred. No.
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the methods
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commendation relates to a novel gene therapy composition comprising a commendation one saidoprotein (asp) prometer operably linked to a gene espence encoding a toxic and/or therapeutic protein contained within a condition of the process gene expression in tissue and tumour cells with containing the toxic gene expression in tissue and tumour cells with containing the toxic protein contained within a calcification potential, it is active in fully-differentiated osteoblasts of hone, in trophoblastic cells of the placenta, and in cementum and contain of teeth. It is also active in a vuriety of human tumours or the placenta and increment and the containing the composition of the invention may be used to treat estection the containing the composition of a gene encoding a protein such as processed of expression of a gene encoding a protein and a placent protein and a containing the composition of the containing a protein and a containing the containing the containing to the containing to the containing the containing
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288888888888888888888888888888888888

Sequence 2421 BP; 891 A; 438 C; 425 Ģ 667 T; 0 other;

Best Loc Matches Query Match 30; Similarity Conservative (100.0%; 0, Score Pred. Mismatches No. 0.015; 0 Length 2421; Indels 0; Gaps

0

RESULT 3 AAS53160

묽 S

1487 ATATAGAAGCCCAAGAAAAATCAGCTGACC 1516

ATATAGAAGCCCAAGAAAATCAGCTGACC 30

AASS3160 standard; DNA; 2577

13-FEB-2002 (first entry

Enterococcus faecalis DNA for cellular proliferation protein #588.

Antisense; ds; prokaryotic cellular proliferation gene antibacterial; drug design.

Enterococcus faecalis

WO200170955-A2

27-SEP-2003

21-MAR-2001; 2001WO-US09180. 2000US-191078P. 2000US-206848P. 2000US-207727P.

21-MAR-2000; 23-MAY-2000; 26-MAY-2000; 23-OCT-2000; 27-NOV-2000; 2000US-242578P. 2000US-253625P. 2000US-257931P. 2001US-269308P.

(BLIT-) ELITRA PHARM INC

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AAX12984/c
ID AAX129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or the invention relates to antisense inhibitors of gense sesential to probaryotic ceillular proliferation, their use in identifying the gense sheets their use in the discovery of novel antiblotics, the essential occupies these less that need discovery of novel antiblotics, the essential occupies these pseudomona antiblotics and proceed the process of the second state of the second proteins. The proceduration of potential new targets of invention is also useful for the identification of potential new targets of or antiblotic development. The antisance models cade son also be used to consider the identification of potential new targets of or antiblotic development. The antisance models cade son also be used to consider the second of the procedure of the antisense models and sequence is also useful to occase the procedure and the useful to coronate occase and the procedure of the procedure and the sequence of the procedure of the procedure of the sequence of the procedure of the 
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Best Local S
Matches 24
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06-MAY-1997;
16-MAY-1997;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis genome contig SEQ ID NO:47.
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                        WPI; 1999-045171/04
                                                                                                                                                                                                                                                                                      04-MAY-1998;
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                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                        12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus
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                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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                                                                          Dillon PJ,
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Xu HH;
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97US-0044031.
97US-0046655.
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                                                                              Kunsch CA;
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Pred. No. 21;
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New isolated Enterococcus facealis polymodactides and polypeptides

- used to develop products for the detertion of Enterococcus and for

use in accines for prevention or attenuation of Enterococcus
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Claim 1; Page 429-438; 2084pp; English.

primary much oritic sequences, also known as contigs. The computer-based bytems can identify fragments of the Enterocongue faccalis (genome with owners) in importance. The products can be used to detect the presence of Enterocongue faccalis in samples. They can also be used for designosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcas faccalis, or another related organism, in two or in vitro. In particular the polypeptides encoded by the Enterococcas faccalis uncleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal A computer readable medium has been developed which has recorded on 982 nucleotide sequences isolated from the Entercoccus faecalis ger AMX12338 to AMX13919 represent these nucleotide sequences which are genome

rfffkkkkinnnnnnn

Sequence 17087 BP; 4734 A; 3683 C; 3245 ç, 5415 T; 10 other;

Matches Best Query Match Local 4 TAGAAGCCCAAGAAAATCAGCTGACC 30 24; Similarity Conservative 88.9%; 74.0%; 0; Pred. Score Mismatches No. 2 В 20; <u>ω</u> Length 17087; 0; Gaps

0

11327 TAGAAGCCGAAGAAAAATCAGTTGAAC 11301

S 밁

ABS98779 standard; DNA; 17087

ABS98779

18-DEC-2002

Enterococcus faecalis contig sequence #47 (first entry)

RESULT 5
ABS98779/c
ID ABS98779/c
XX 18-D80977
XX 18-D80
XX 18-D80
XX 28-D80
XX 28-D80 pathogenicity; vaccine; resistance; Entercoccal infection; commercial; therepautic; industrial; fermanting; sugar source; metabolic; vaccine; slochip technology; antibacterial; modulator of nucleic acid expression; contig; ds. Computer readable medium; Enterococcus faecalis; microbe; growth;

Enterococcus faecalis

US2002120116-A1

04-MAY-1998; 98US-0070927.

04-MAY-1998; 9805-0070927

(KUNS/) KUNSCH C A. (DILL/) DILLON P J. (BARA/) BARASH S.

Kunsch P Dillon PJ, Barash ģ

XZZZZZZ

Computer readable medium having recorded on it a Enterococcus nucleotide sequence useful for detecting diseases related to WPI; 2002-750065/81.

Claim 1; Page -; 119pp; English Enterococcus infections

in animals

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RESULT 6
ABA05477
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Matches 24
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The invention relates to human RWA gyrase 12, the polymuclectide encoding this polyepride and NNA recombinant techniques to produce the applying polypeptide. The present invention also discloses a method of applying this polypeptide to treat various diseases, such as malignant tumour,
                                                                                                                                                                                                  New polypeptide-human RNA unwindase 12 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN1311325-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; RNA gyrase 12; malignant tumour; haemopathy; HTV; infection;
human immunodeficiency virus; immunological disease; inflammation;
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                                                                                                                                            Claim 6; Page
                                                                                                                                                                                                                                                                                        WPI; 2002-049927/07
P-PSDB; AAM47948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000; 2000CN-0111862
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                                                                                                                                            25-26 (Disclosure); 33pp; Chinese.
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467..802
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/product= "RNA gyrase 12"
/note= "claimed in claim 6"
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Pred. No. 2
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                                                                                                                                                                                                                                      and polynucleotide encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
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The invention relates to a nucleic acid comprising a sequence of 18 hases, of a sequent of chemically pretreated max (or publ) e.g. with bisulphile, of genes associated with tumour suppression and concepted sharing a sequence taken from 536 (activally 53) since concepted sharing a sequence taken from 536 (activally 53) since concepted sharing a sequence taken from 536 (activally 53) since concepted and so are missing from the sequence listing sequences (S8) and sequences complementary to (S8). The nucleic acid may be a capable from part of a set of probes for detecting the nucleotides and may complementary to (S8). The nucleic acid may be a capable from the sequence sharing the sequence of the probes for detecting the cytosism eachlylation state candors single mucleotide polymorphisms and also to be used in a method for capable from the sequence in the diagnosis and compared to another set of genetic parameters for the diagnosis candors that any of sequence and the secretary and the secretary because of the prediction to specific confidence acriving as battlet or flag research sequence is one of the state of the sequence are one of the sequence as sequence are one of the sequence as sequence are one of the sequence are one of the sequence are of the sequence are one of the sequence are of the sequence are of the sequence are one of the sequence are one of the sequence are of the sequence are one of the sequence are of the sequence are one of the sequence are of the sequence are one of the sequence are one of the sequence are of the sequence

Pragments of chamically modified gense associated with tumour suppressor gense and oncogense, useful in designing primares and probes for analysing diseases associated with cycosine methylation state e.g.

Claim 1; SEQ ID No 411; 27pp; English.

Olek A,

Piepenbrock

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WPI; 2001-602752/68

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RESULT 7
NAS46688/c
ID NAS466
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Best Local
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                                                                                                                                                                                                                                                          15-MAR-2000; 2000DE-1013847
06-APR-2000; 2000DE-1019058
07-APR-2000; 2000DE-1019173
30-JUN-2000; 2000DE-1032529
                                                                                                                                                                                                                                                                                                                                                             cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                    Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         AAS46688
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS46688 standard;
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                                                                                                                                                                                                                                                                                                                                                                                          Tumour suppressor gene derived chemically modified sequence
                                                                                                                                                                                                                                    (EPIG-)
                                                                                                                                                                                                                                                                                                15-MAR-2001; 2001WO-EP02955
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                     EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 6816 BP
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene, liver cancer; ds; hepatocellular carcinoma hepatotropio metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug coxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogenes.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                              expression of two or more genea represented in ABM9303-ABM97455 in a tissue sample. The method of the invention has bepartorroot, and optomization activity. The method is useful for diagnosing and detending the progression of liver cancer, hepstocellular curcinoma and metastatic liver carcinoma, in a patient. The method is useful for identifying as markers that can be used to monitor disease times, disease progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200229103-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene #2407 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6816 BP; 1903 A; 67 C; 1504 G; 3338 T; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
Sequence 3610 BP; 1322 A; 622 C; 963 G;
                                                                                 drug toxicity, drug efficacy and drug metabolism. Mote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO
                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocallular carcinoma or metatatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatoceallular carcinoma in a patient, and afferentiating metastatic liver cancer from hepatoceallular carcinoma in a patient, involving detecting the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biagnosting and detecting the progression of liver cancer, hepatocellular carcinome or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horne D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2000; 2000US-237054P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   liver tissue sample
                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6609 ATATAAAACCCAAAAAAAAATCACCTAACC 6580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; SEQ ID NO 2407; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATATAGAAGCCCAAGAAAATCAGCTGACC 30
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Pred. No. 1.2e
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703 T; 0 other;
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Query Match

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                                                                                                                                                                                                                                                    02-0CT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2001; 2001WO-US10838
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27-SEP-2000;
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2000US-235863P.
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2000US-237608P
2000US-244867P
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2000US-237604F.
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2000US-237316P.
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RESULT 10
ABL68604
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Best Local S
Matches 23
05-JWH-2000; 2000WS-209473P

05-JWH-2000; 2000WS-209531P

18-SEP-2000; 2000WS-233133P

18-SEP-2000; 2000WS-234603P

20-SEP-2000; 2000WS-234603P

20-SEP-2000; 2000WS-234032P

20-SEP-2000; 2000WS-234032P
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Soppet DR,
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kidney cancer related gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
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82.1%;
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Pred. No.
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ches 5;
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(AVAL-) AVALON PHARM.

Augustus M, Weaver Z; Carter KC, Ebner R, Endress G, Horrigan ģ

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing calls to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set

Claim 1; SEQ ID 6941; 44pp; English

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical capent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (8) selected from 8447 sequences (given in ABIG1664 or ABIG101), or is an Least 95' Mederical, or (8), where a change in the compression of an anti-neoplastic agent, and can be the plant in a to be used for screening capent, and can be used for producting a product which cape is the data collected with respect to the anti-neoplastic agent as a convey the chemical capent is the data of caper such as colon, breast, remach, lung, thyroid, ceepingsel, overlan, kidney, prostate or pancreatic cancer.

Converted to cancer such as colon, breast, remach, lung, thyroid, ceepingsel, overlan, kidney, prostate or pancreatic cancer. infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine papillary carcinoma and Wilm's tumour.

Sequence 3610 BP; 1322 A; 622 C; 963 G; 703 T; 0 other;

Query Match
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Matches 23; Conserv Conservative 66.7%; 0, Score 20; Pred. No. Mismatches DB 24; L-1.6e+02; 5; Length 3610; Indels ٥, Gaps

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                                                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developments bology and in cluvidating cell signaling and coll-cell interactions in higher entaryones for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (BELG17-3BEJ0511), expressed DNA sequences (BELG17-3BEJ0511) expressed DNA sequences (BELG17-3BEJ0511).
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11-JUL-2000; 2000US-0614150
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pharmaceutical; gene; ds.
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  Genomic sequence of Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                              Sequence 5088 BP; 1622 A; 1000 C; 938 G; 1528 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 3187; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting genes from Drosophila and for elucidating cell signalling
                                16-MAY-2002
                                                                                           ABA90521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent
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(ABB57737-ABB72072)
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                                                                                           standard; DNA; 2365589 BP
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21-DEC-1999;
14-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                          Cervical cancer;
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99US-0169681.
99US-0171350.
2000US-0189315.
2000US-0203791.
2000US-0220600.
2000US-0220114.
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Matches 22
The invention relates to novel genes (AMB69727-AM17383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful; to assess if a patient is afflicted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (AAM69727-AAM7383) associated with cervical cancer with cycostatic activity. The muchic acids and encoded polyoperiodes are useful: to assess if a patient is affilicted with corvical cancer or has a pre-malignant condition, to monitor the progression of cervical cancer or a premalignant condition in a patient; and resolved and/or sesses the efficacy of a compound or thought for thinitioning cervical cancer in a patient. The molabel acids may also be
                                           Claim 1; Page 215-216; 1051pp; English
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAH69370 standard; cDNA; 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 508 BP; 108 A; 143 C; 129 G; 128 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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                                                                                                  WPI; 2001-375006/39.
                                                                                                                     Schlegel R,
                                                                                                                                                                                                                          08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                             (MILL-)
                                                                                                                                                                                                   14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated nucleic acid for diagnosing and treating cervical cancer
                                                                            isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 TAGAGAAGCCCAAGAAGTAGCAGCTG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for gene therapy.
                                                                assessing and
                                                                                                                                            MILLENNIUM PREDICTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assessing and detecting
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                                                                                                                                                                           2000US-0189315.
2000US-0203791.
2000US-0210600.
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                                                                                                                     Deeds J,
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                                                                                                                                                                                                                        9908-0169681
                                                                                                                                                                                                                                                                                                                                cytostatic;
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84.6%;
                                                              acid for diagnosing and treating cervical cancer -
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                                                                                                                                                                                                                                                                                                                                pre-malignant condition; gene therapy;
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                                                                                                                                            MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                       Zhao X;
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progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                          cervical cancer or has a pre-malignant condition; to monitor the
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Sequence 539 BP; 118 A; 152 C; 137
  G; 132 T;
     0 other;
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Query Match
Best Local S
 22;
        Similarity
 Conservative
        84.6%;
0;
      Score 19.6;
Pred. No. 1.
 Mismatches
        1.96+02
              띪
              22;
 Indels
             Length
 0
Gaps
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152
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TAGAGAAGCCCAAGAAGTAGCAGCTG 127
                              TATAGAAGCCCAAGAAAAATCAGCTG 27
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Human cervical cancer marker nucleic acid 2446
                            19-SEP-2001
                                                         AAH71172;
                                                                                 AAH71172
                                                                                 standard; cDNA;
                          (first entry
                                                                                 547
                                                                                   Въ
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Cervical cancer; Homo sapiens cytostatic; pre-malignant condition; gene therapy; ss

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08-DEC-2000; 2000WO-US33312
                                                                                         WO200142467-A2
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14-MAR-2000; 12-MAY-2000; 09-JUN-2000; 21-DEC-1999; 21-JUL-2000; 99US-0171350. 2000US-0189315. 2000US-0203791. 2000US-0210600. 2000US-0220114

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC

08-DEC-1999;

9908-0169681

WPI; 2001-375006/39. Schlegel × Deeds J, Berger A, Zhao X;

isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer

Page 513; 1051pp; English.

The invention relates to novel genes (AMH89727-AMH7388) associated with cervical cancer with cytocetaic sectivity. The nucleic acids and encoded polyappitics are useful; to assess if a patient is afflicted with cervical cancer or has a premailignant condition. To motifor the progression of cervical cancer or a premailignant condition in a patient; and to estect and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The motiform cards may also be usetul for gene therapy.

Seguence 547 BP; 119 A; 153 C; 142 G; 133 T; 0 other;

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S
                         Query Match
Best Local :
                 Matches
                          Similarity
 TATAGAAGCCCAAGAAAAATCAGCTG
                         65.3%;
                 0;
                         Score 19.6;
Pred. No. 1
                  Mismatches
  27
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                  Indels
                                Length 547;
                  0
                 Gaps
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161

TAGAGAAGCCCAAGAAGTAGCAGCTG

Search completed: December 18, 2003, 10:29:56 Job time : 203.721 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 09:02:17 , Search time 43,7705 Seconds (without alignments) 302.521 Million cell updates/sec

Sequence: Title: Perfect score: US-09-889-491-13 30 1 atatagaagcccaagaaaaatcagctgacc 30

Scoring table: Gapop 10.0 , Gapext 1.0

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569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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11 /cgg72 6/prodate/2/ina/5A COMB.seq;*

21 /cgg72 6/prodate/2/ina/5B COMB.seq;*

21 /cgg72 6/prodate/2/ina/6B COMB.seq;*

4 /cgg72 6/prodate/2/ina/6B COMB.seq;*

4 /cgg72 6/prodate/2/ina/6B COMB.seq;*

5 /cgg72 6/prodate/2/ina/backfitsi.seq;*

6 /cgg76 6/prodate/2/ina/backfitsi.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIBS

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Sequence 1, Appl. Sequence 1822, Appl. Sequence 13, Appl. Sequence 78, Appl. Sequence 5, Appl. Sequence 1, Appl. Sequence 1, Appl.	387 e 1, 1, 189	189, 37, 37, 129,	1,62,831	Description Sequence 4, Appli Sequence 4, Appli

4 4	3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
17	17	17	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2
56.7	56.7	56.7	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3	57.3
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US-08-998-416-289 US-09-453-702B-189	US-08-998-416-1138	US-08-998-416-187	US-09-198-452A-1	US-09-173-914-6	US-08-961-527-61	US-08-738-349-5	US-08-738-349-3	US-08-580-031A-4	US-08-332-638-57	US-08-332-643-51	US-08-188-228-57	US-09-252-991A-1417	US-09-328-352-507	US-09-252-991A-1191	US-09-381-849-6	US-08-716-301-5
Sequence 189, App		Sequence 187, App	Sequence 1; Appli	Sequence 6, Appli	Sequence 61, Appl	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 57, Appl		Sequence 57, Appl	Sequence 1417, Ap	Sequence 507, App	Sequence 1191, Ap	Sequence 6, Appli	Sequence 5, Appli

ALIGNMENTS

IOCATION: 2050 4053	; NAME/KEY: CDS	; FEATURE:	MODELONE TIES: DAM (SCHOOLTC)	TVDE . DAY	2	; STRANDEDNESS: single	O	; LENGTH: 6854 base pairs	SEQUENCE CHARACTERISTICS:	INCOMMATION FOR SEQ ID NO: 4:	TO SEC TO NO.	2	; TELEFAX: 312/474-0448	; TELEPHONE: 312/474-6300	P	REFERENCE DUCKET NOMBER: 2/866/31/84	7	300	NAME: NO 5729806and Grata E	N-199	APPLICATION NUMBER: US 08/184,605	_	; CLASSIFICATION: 530	; FILING DATE: 06-JUN-1995	; APPLICATION NUMBER: US/08/468,036	LICATION DATA:	Patent	; OPERATING SYSTEM: PC-DOS/MS-DOS	COMPUTER: IBM PC compatible	靐	606-6402	ĸ	••	Chicago	300 Sears Tower, 233 South Wacker Drive	ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun	33	F SEOUENCES: 48	OF INVENTION: Interact with Casein Kinease I	NVENTION: N	Hoekstra, Merl F.	APPLICANT: DeMaggio, Anthony J.	: Patent No. 5728806	RESULT 1

Query Match

64.7%; Score 19.4; DB 1; Length 6854;

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                                              Sequence 17, Application US/08441139 Patent No. 5773245
                                                                                                                                                                                                                  Matches
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Best Local
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                               GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 6854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: No. 5846764and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Hockstra, Merl F.
TITLE OF INVENTION: Metrials and Methods Relating to Proteins
TITLE OF INVENTION: that Interact with Casein Kinase I
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                  PEATURE:
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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PRIOR APPLICATION NUMBER: US 08/184,605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Raiann "
                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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TELEFAX: 312/474-0448
TELEX: 25-3856
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
Wittrup, Dr. Karl D.
Robinson, Anne S.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4366

TELEPHONE: 516-742-4366

TELEPK: 200 901 SANS UR
INFORMATION POR SBO ID NO: 17:
SEQUENCES CHERACTERISTICS:
LENGTH: 2400 beep paire
                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38, Application US/08468036 Patent No. 5728806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Hoekstra, Merl F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPES, Flogpy disk
COMETTER: IN PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTNARS: FatentIn Extense #1.0, Version #1.25
CURRENT APPLICATION DAYA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
COMPUTER: ISM FO COMPARTING
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PStentin Re-lease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 06-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Garden City
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 15-MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                   ZIP: 60606-6402
                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 11530
                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
                    APPLICATION NUMBER:
                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1929 AGAAGCCCAGGAAAAAGCTGCTGA 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AGAAGCCCAAGAAAATCAGCTGA 28
                                                                                                                                                                                                        Chicago
                                                                                                                                                                                                                         B: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECOMBINANTLY EXPRESSED PROTEINS
                                                                                                                                                                                                                                                                                                   Materials and Methods Relating to Proteins that Interact with Casein Kinease I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS FOR INCREASING SECRETION OF
                                                                                                                                                                                                                                                                                 48
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                 US/08/468,036
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Pred. No. 39;
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                                                       Version #1.25
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FILING DATE:

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US-08-376-843-38/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5846764
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3466 base pairs
                                                                                                                 APPLICATION NUMBER: US 08/184,605
PILLING DATE: 02-13A1-194
AUTHORNET/ARENT INFORMATION:
NAME: No. 2446764and Green B.
RESIETRACTION NUMBER: 35,202
REFERENCE/DOCTET NUMBER: 27866/3178
TELECOMUNICATION INFORMATION:
TELECHONE: 313/474-4500
TELECHONE: 313/474-6500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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LENGTH: 3466 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DeMaggio, Anthony J. APPLICANT: Hoekstra, Merl F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: Materials and Methods Relating to Proteins ITLE OF INVENTION: that Interact with Casein Kinase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 64.0%;
Local Similarity 87.5%;
                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: No. 5728806and,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 ATAGAGAAGCCGAAGGAAAATCAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                US/08/376,843
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Cower, 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                             27866/31784
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Pred. No. 41;
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South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3466;
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US-08-376-843-38
                                        US-08-686-878A-8/c
                                                                                                                                                                                                                  ; ORGANISM: Oryza sativa
US-08-728-956-2
                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-728-956-2
           Sequence 8, Application US/08686878A Patent No. 5708157
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                       Query Match
Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (317)231-7433
(NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMFUTER: REMANDALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ITM FC Compatible
OPERATING SYSTEM: 9C-000/M9-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)231-7745
TELEPAX: (317)231-7433
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hodges
APPLICANT: McGee,
                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 11 S Merid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                BNGTH
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                                                                                                   292 TTGAAGCAGAAAAAAGCAGCTGAGC 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                         22;
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                                                                                                                            4 TAGAAGCCCAAGAAAATCAGCTGACC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION: Plant Pathogen Induced Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indiana
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11 S Meridian
                                                                                                                                                                                                                                                                                                                                              613 base pairs
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                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                     DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.0%;
                                                                                                                                                                       63.3%;
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Pred. No. 41;
                                                                                                                                                                       Score 19;
Pred. No.
                                                                                                                                                           Mismatches
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                                                                                                                                                                       DB 1;
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                                                                                                                                                                                      Length 613;
                                                                                                                                                           Indels
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APPLICANT:

Jacobs, Kenneth McCoy, John

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US-09-175-928-13/c
                                                      NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09175928A Patent No. 6312921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                   MEPLICANT: discobs, Kenneth
APPLICANT: MCCOS, Kenneth
APPLICANT: LAVALIA: Behard R.
APPLICANT: LAVALIA: Debard R.
APPLICANT: PARALLIA: ALSA A.
APPLICANT: PRANS, Cheryl
APPLICANT: Prascy, Maurice
APPLICANT: Moresty, David
APPLICANT: Moresty, David
APPLICANT: Genetic Institute, Inc.
APPLICANT: MORESTY ON MORESTY OF PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
TILLS REFERENCE: 60065.AJ172A
CURRENT APPLICATION MOREST: 1096-10-20
CURRENT APPLICATION MOREST: 1096-10-20
CURRENT APPLICATION MOREST. 1096-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTOONEY/AGENT IMPORATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
RELECOMONNICATION IMPORBATION:
TELEBOOMEN (AT) 1976-88-124
TELEBOMEN: (617) 498-824
TELEBOM: (617) 4976-88-12
TELEBOM: (617) 676-88-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 876-585
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Computible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PSECULION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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                                         ENGTH: 429
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APPLICANT: SPAULDING YELKH
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 TACAGAAGCCCAAGAAAGAGCAAGAGAC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TATAGAAGCCCAAGAAAAATCAGCTGAC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
22; Conserv
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merberg, L. Maurice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LaVallie, Edward
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Pred. No. 62;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                         PRIOR DEPLICATION DATA:
APPLICATION NUMBER: 06/027,032
APPLICATION NUMBER: 06/027,032
APPLICATION NUMBER: 196
APPLICATION NUMBER: 1800
APPLICATION NUMBER: 38,091
ARTERINGE/DOCCET NUMBER: 50549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KBY: unsure
LOCATION: (24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FRANCES for Windows Version

CURRENT APPLICATION DATA:

THE TOTAL ACT ACE
                                                                                                                                                                                                                                                                                                                                             ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilme Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPIJICANT: Resichard, Richard
APPIJCANT: Resemberg, Martin
APPIJCANT: Ward, Judith
APPIJCANT: Ward, Judith
TITIE OF INVENTION: No. 6348592el Prokaryotic Polymucleotides.
TITIE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION:
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                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189, Application US/08936165A
5. 6348582
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   610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knowles, David
Lonetto, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burnham, Martin
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PS0549

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Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                        NAME/KEY: unsure
LOCATION: (142)..(143)
                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (18)..(19)
333 TÁCAGÁAGCCCAAGAAAGAGCAAGAGAC 306
                     2 TATAGAAGCCCAAGAAAAATCAGCTGAC 29
                                              Conservative
                                                        78.6%;
                                              °,
                                                        Score 18.4;
Pred. No. 62;
                                              Mismatches
                                                                       DB 4;
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                                                                       Length 429;
                                                Indels
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Best Local Similarity 75.9
Matches 22; Conservative
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Patent No. 6498022
                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                      Sequence 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WEI, MING-HAL de al.
TITHE OF INVENTION: SOLATED HUMAN TRANSPORTER PROTEINS,
TITHE OF INVENTION: AUCUSIC ACID MOLECULES ENCODING HIMAN TRANSPORTER PROTEINS,
TITHE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOIOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(202001)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 202001
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                         APPLICANT: Hodgeon, John
APPLICANT: Kloovles, David
APPLICANT: Kloholas, Richard
APPLICANT: Stodola, Robert
APPLICANT: Stodola, Robert
APPLICANT: Stodola, Robert
MITHLE OF INVENTION: No. 6348328el Compounds
MINDERS OF SEQUENCES: 525
                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 170709 ATATAGAAGTCAAATGAACATCAGTTGA 170682
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STRANDEDNESS: single
                                                   COUNTRY:
                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                  7, Application US/08858207A 6348328
                                                                                  King of Prussia
                                                                    PA
                                                                                                         709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1355 base pairs
                                                      USA
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Diskette
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Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Pred. No. 1.6e+02;
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  SEQUENCE CHARACTERISTICS:
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RESULT 12
US-07-792-865D-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
TELEPAX: (212) 753-6237 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          COMPUTER: IBM OF IBM-OO
OPERATING SYSTEM: PC/MS
SOFTWARE: WOOTOPETECT
CURRENT APPLICATION UNDER: US/
APPLICATION UNDER: US/
FILING DATE: 19911004
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LENGTH: 2179 base pairs
TYPE: nucleic acid
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NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
                            NAME: Jackson, Arthur REGISTRATION NUMBER: 34,354 REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
                                                                                                                APPLICATION NUMBER: PCT/US: FILING DATE: April 3, 1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: THE APICAL END OF THE PARASITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: John W. B. APPLICANT: Samuel P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PSTELECOMMUNICATION INFORMATION: 10-270-4478
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
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FILING DATE: 14-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                       B: Darby & Darby P.C.
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                              IBM or IBM-compatible
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                                                                                                                                                                                                                                                                                                                     Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barnwell, Mary W. Galinski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%; Score 18; DB 4;
80.8%; Pred. No. 1.2e+02.
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                                                                                                                                                                                                                                                                                   PC/MS-DOS
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Best Local S
Matches 21
                                                                                                                                                                         Sequence 129, Application US/08961527 Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                -07-792-865D-1
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: Lambda gt 11 nat:
LIBRARY: DNA expression 1:
CLONE: 5.3
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
COMPUTER READABLE FORM
                                                                                    ADDRESSEE: Human Gen
                                                                                                                                APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
DESCRIPTION:
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CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                             COUNTRY:
                                                         STREST: 9410 Ke
                                                                                                                                                                                                                                                                                                                       Local Similarity 80.8
mes 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: P.vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                971 ATATAGAAGACGCAGAAAAACAAGCT 996
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                  20850
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                                             Maryland
                                                                      E: Human Genome Sciences, Inc
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3763 base pairs
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                                                                                                                                                                                                                                                                                                                                  80.83;
                                                                                                                             Streptococcus pneumoniae Polynucleotides and Sequences
                                                                                                                    391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence corresponds to
Figure 1A (sheets 1-4) in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     application, as filed.
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Pred. No. 1.3e+02;
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RESULT 15
US-09-671-317-387
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; Sequence 387, Application US/09671317
                                                                                                                                                                                                                                 US-09-685-853A-3
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                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09685853A
Patent No. 6479270
                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/685,853A
CURRENT FILING DATE: 2002-05-06
FRIOR APPLICATION NUMBER: 60/182,194
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPLICANT: WEI, Ming-Hal et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
FILE EEPERGNUE: CLOOOF)1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCY/DOCKET NUMBER: 99.4
TELECOMMUNICATION INFORMATION:
TELEPHONE; (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(74962)
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 48
OPERATING SYSTEM: MEDI
SOPTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                       ENGIH: 74962
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LENGTH: 8512 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US
                                                                                                                                                                          Local Similarity
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                                                                                       74050
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                                                                                                                        1 ATATAGAAGCCCAAGAAAATCAGCT 26
                                                                                                                                                         21;
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EDNESS: double
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                                                                                     ATTTANGAGCCCATGAAAAGTCAGCT 74025
                                                                                                                                                            Conservative
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NSTEM: MSDOS version 6.2
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                                                                                                                                                                          60.0%;
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80.8%;
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Pred. No. 1.5e+02;
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                                                                                                                                                                                             Score 18;
                                                                                                                                                         Mismatches
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                                                                                                                                                                            2.1e+02;
                                                                                                                                                                                             DB 4;
                                                                                                                                                                                          Length 74962;
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                                                                                                                                                         Gaps
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NAME/KEY: misc_feature
LOCATION: 24,736,739
JOTHER INFORMATION: n=a, g, c or t
US-09-671-317-387
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; SEQ ID NO 387
; LENGTH: 1000
; TYPE: DIAA
; ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_binding
LOCATION. 472-486
OTHER INFORMATION 12-662-80.misl, potential
NAME/KEY: misc_binding
LOCATION. 489.517
DIRECTION. 499.517
D
                                                                                                                                   Query Match 59.3
Best Local Similarity 75.5
Matches 22; Conservative
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PRIOR PRIOR PRILING DATE: US 60/131,961
PRIOR PLILING DATE: 1990-04-30
WIMBER OF ESD ID NOS: 977
NO TO YOUR PRINCE PRINCE
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APPLICANT: Chemakov, 11/4.

APPLICANT: BROUND-RESEL, LVd1s-
APPLICANT: BROUND-RESELL LVd1s-
APPLICANT: BROUND-RESELL COMPANIES TO GENES INVOLVED IN DRUG METABOLISM
TITLE OF INVENTION: SIALLELIC MAXERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
TITLE OF INVENTION NUMBER: US/09/671,317
CURRENT EPILICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
ERIOR APPLICATION MUMBER: US/09/671,317
SEXOR FILING DATE: 2000-09-27
BRIOR APPLICATION MUMBER: W50-912/1800/00-469
PRIOR APPLICATION MUMBER: US-80/126,269
RRIOR APPLICATION MUMBER: US-80/126,269
RRIOR APPLICATION MUMBER: US-80/126,269
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NAME/KRY: Allele
LOCHTION: 1497
COTHER INFORMATION: 12-662-80 : polymorphic base G or C
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1 ATATAGAAGCCCAAGAAAAATCAGCTGAC 29
                                                                                                                                                                                                                       59.3%; Score 17.8; 75.9%; Pred. No. 1.
                                                                                                                                               0,
                                                                                                                                               Mismatches
                                                                                                                                                                                                                       DB 4; Length 1000;
                                                                                                                                                           Indels
                                                                                                                                               · 0;
                                                                                                                                               Gaps
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Search completed: December 18, 2003, 09:04:15 Job time: 49.7705 secs

971 ATGTAGAAGGACAAGAAAAAAAGGTTGAC 999

OM nucleic - nucleic search, using sw model 600 December 18, 2003, 09:02:17; Search time 965,902 Seconds (without allignments) 103.495 Million cell updates/sec

Sequence: Perfect score: US-09-889-491-13 30

Scoring table: 1 atatagaagcccaagaaaaatcagctgacc 30

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: Searched: 2211978 seqs, 1666101734 residues 4423956

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:*

1 /cgn2 6/ptodata/2/pubpna/US07
2 /cgn2 6/ptodata/2/pubpna/PCT N
3 /cgn2_6/ptodata/2/pubpna/US06
3 /cgn2_6/ptodata/2/pubpna/US06 PUBCOMB.seq:*
I NEW PUB.seq:*
06 NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5 19.2	4 19.2	3 19.2	2 19.2	1 19.2	0 19.4	9 19.6	8 19.6	7 20	6 20	5 20	4 20.4	3 20.4	2 22.2	1 22.2	t Score
64.0	64.0														!
20561	2169	1695	837	837	406	52354	405	3702	3610	3610	1923	1923	17087	2577	Query Match Length DB
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US-09-070-927A-292	US-09-815-242-6699	US-10-032-585-6149	US-10-027-632-147079	US-10-027-632-147079	US-09-815-343-1379	US-09-742-311-3	US-09-918-995-36137	US-10-084-817-30	US-09-873-367C-721	US-09-880-107-2406	US-10-027-632-255052	US-10-027-632-255052	US-09-070-927A-47	US-09-815-242-6797	ID
Sequence 292, App	Sequence 6699, Ap	Sequence 6149, Ap	Sequence 147079,	Sequence 147079,	Sequence 1379, Ap	Sequence 3, Appli	Sequence 36137, A		Sequence 721, App	Sequence 2406, Ap	Seguence 255052,	Sequence 255052,	Sequence 47, Appl	Sequence 6797, Ap	Description

LENGTH: 2577 TYPE: DNA ORGANISM: Enterococcus faecalis

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18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.8		18.8	18.8	18.8	18:8	19	19	19	19
61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.7	62.7	62.7	62.7	62.7	62.7	63.3	63.3	63.3	63.3
441	441	441	441	429	429	405	296	285	261	261	218	10046	10046	7916	673	673	642	642	504	8805	4403	1100	1100	560	133	2174	2174	908	483
14	14	13	13	15	14	10	14	10	11	10	10	15	ø	10	4	ü	14	13	10	5	œ	14	13	15	9	14	13	ø	9
US-10-027-632-182664	US-10-027-632-182663	US-10-027-632-182664	US-10-027-632-182663	US-10-016-249-13	US-10-040-916-8	US-09-938-842A-3609	US-10-114-893-142	US-09-867-701-4769	US-09-822-846-67	US-09-867-701-7801	US-09-867-701-4483	US-10-073-961-458	US-09-764-887-458	US-09-479-040-1	US-10-027-632-285692	US-10-027-632-285692	US-10-027-632-251328	US-10-027-632-251328	US-09-479-040-6	US-09-070-927A-135	US-08-781-986A-78	US-10-027-632-9964	US-10-027-632-9964	US-10-157-031-258	US-09-770-696-601	US-10-027-632-256360	US-10-027-632-256360	US-09-770-445-794	US-09-864-761-6011
Sequence 182664,	Sequence 182663,			13	8,		14	476		780		Sequence 458, App	458	ŗ				251	Sequence 6, Appli	Sequence 135, App	78, Apr	9964,	9964	9 258	Sequence 601, App	256		794, 7	Sequence 6011, Ap

ALIGNMENTS

RESULT 1

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LENGTH: 2577	SOFTWARE: FASTSEQ for Windows Version 4.0	SEQ ID NOS: 14110	PRIOR FILING DATE: 2001-02-16		FILING DATE:	APPLICATION N	: 2000-11	PRIOR APPLICATION NUMBER: 60/253,625	FILING DATE: 2000-10	APPLICATION N	FILING DATE: 2000-05	PRIOR APPLICATION NUMBER: 60/207,727	PRIOR FILING DATE: 2000-05-23	APPLICATION N	PRIOR FILING DATE: 2000-03-21	HUN NOIT	CURRENT FILING DATE: 2001-03-21	CURRENT APPLICATION NUMBER: US/09/815,242	REFERENCE: ELITE	TITLE OF INVENTION: Prokaryotes	W	APPLICANT: Xu, H. Howard	APPLICANT: Yamamoto, Robert T.	APPLICANT: Carr, Grant J.		APPLICANT: Wall, Daniel	APPLICANT: Zyskind, Judith W.	APPLICANT: Ohlsen, Kari L.	APPLICANT: Haselbeck, Robert	GENERAL INFORMATION:	Patent No. US20020061569A1	Sequence 6797, Application US/09815242	US-09-815-242-6797

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RESULT 3
                                                                                            Query Match
Best Local Similarity 88.9
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NAME/KEY:
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                    PPILCATION NUMBER: 60/046,655
PILING DATE: 1997-05-16
PPILCATION NUMBER: 60/044,031
PILING DATE: 1997-10-14
PPILCATION NUMBER: 60/066,009
PILING DATE: 1997-11-14
ATTORNET/LEGET THEYBACATON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 24; Conserv
                                              11327
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 17087 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                 NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE JOCKET NUMBER: P3369
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: HP Vectra 486/33

ORENITING SYSTEM: MSDOS Version 6.2

SOTUMARE: ABCLIT Text

SOTUMARE: ABCLIT Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Charles A. Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
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                                      TAGANGCCGAAGAAAATCAGTTGAAC 11303
                                                                       TAGAAGCCCAAGAAAAATCAGCTGACC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <UNKnown>
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Sg3
                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                      74.0%;
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                                                                                                                        Score 22.2;
Pred. No. 37;
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Pred. No. 2
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                                                                                                                                        DB 10;
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                                                                                                         Indels
                                                                                                                                     Length 17087;
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; ORGANISM: Human
US-10-027-632-255052
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CURRENT PLING BATS, 2002-04-30
PRIOR MPPLICATION WINBER: US 60/218,006
PRIOR PLING BATS, 2000-07-12
PRIOR MPPLICATION WINBER: US 60/198,676
PRIOR MPLICATION WINBER: US 60/198,483
PRIOR MPLICATION WINBER: US 60/193,483
PRIOR PLING MINBER: US 60/185,218
PRIOR MPPLICATION WINBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 255052, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
ITTLE OF INVENTION: destriction and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE:
                                                                                                SEQ ID NO 255052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mang, David G.
ITILE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                       SOFTWARE: FastSEQ
                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
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                                                                                                                       for Windows Version 4.0
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Pred. No. 1
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                                                                                        CURERRY APPLICATION NUMBER: US/09/873,367C
CURERRY FILING DATE: 2003-04-129
FRIOR REPLICATION NUMBER: U.S. 60/236,891
FRIOR FILING DATE: 2000-09-29
FRIOR REPLICATION NUMBER: U.S. 60/236,842
FRIOR FILING DATE: 2000-09-29
FRIOR REPLICATION NUMBER: U.S. 60/244,867
FRIOR FILING DATE: 2000-11-01
FRIOR FILING DATE: 2000-11-01
FRIOR FILING DATE: 2000-11-01
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Publication No.
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LENGTH: 3610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENERAL INFORMATION:
                                       NUMBER OF SEQ ID NOS: 1067
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR RIPLICATION NUMBER: US 60/211,379
PRIOR FILING BATE: 2000-06-14
PRIOR REPLICATION NUMBER: US 60/237,054
PRIOR FILING BATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Gene Expression Profiles in Liver Cancor
FILE REFERENCE: 44921-5028-09
CURRENT APPLICATION UNMERR: US/99/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using TITLE OF INVENTION: Signature Gene Sets FILE REFERENCE: 689290-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Endress, Gregory
Augustus, Meena
Ebner, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carter, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vockley, Jos
Scherf, Uwe
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Pred. No. 2.2e
0; Mismatches
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Pred. No. 1.4e+02;
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2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                      SERICANT CONTROL NOTE NOTES ACID SEQUENCES OFF TITLE OF INTERTION, NOTE NOTES CONA LIBRARIES OFF TITLE OF INVESTICAN, ERON VARIOUS CONA LIBRARIES CIRERRY APPLICATION NUMBER: US/09/918,995 CIRERRY PAPLICATION NUMBER: US/09/235,076 PRIOR REPLICATION NUMBER: US/09/235,076 PRIOR SEQ ID NOS: 38004 SEQ ID NOS: 3802 ID NOS: 3802 ID NO 36137 PRIOR SEQ ID N
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US-10-084-817-30
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; ORGANISM: Homo sapiens
US-09-873-367C-721
                                                                                                                       US-09-918-995-36137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-918-995-36137
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Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/10084817 Publication No. US20030119009A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36137, Application US/09918995 Fublication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 365
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CURRENT FILING DATE: 2002-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Susan Stuart
APPLICANT: Jed G. Nuch
                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3702
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23; Conser
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        Conservative
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                              65.3%;
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Pred. No.
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Score 20; DB 13;
Pred. No. 2.2e+02;
                 Length 3610;
0
Gaps
0,
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, NAME/KEY: misc feature , OTHER INFORMATION: Incyte ID No. US20030119009A1 1312325CB1 US-10-084-817-30 APPLICANT: Joed G. Machtern APPLICANT: JOEGN M. Shobet APPLICANT: JOEGN M. Shobet TITE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION FILE REPERENCE: PA-0046 US DB 15; Length 3702;

ed. No. 2.2e+02; Mismatches 5 ٥, Gaps

0

OBTAINED

Score 19.6; DB 13 Pred. No. 2.2e+02; 0; Mismatches 4 DB 11; Length 405; 0, Gaps

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RESULT 11
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                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1379
LENGTH: 406
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Best Local Similarity
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SEQ ID NO 3
LENGTH: 52354
                                                                                                                           Matches
                                                                                                                                                          Query Match
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Patent No. US20010055596A1
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                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.504
CURRENT APPLICATION MURRER: US/09/815,343
CURRENT PLING DATE: 2001-03-22
NUMBER OF SEQ ID MOSE .156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Patent No. US20020028773A1
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meagher, Mader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/742,311
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(406)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYTIS OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TYTIS OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TYTLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GUEGLER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(52354)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30034 ACAGATGCTCAATAAAATCAGCTGA 30059
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                                          154 AAATACAAGTACCAGAAAAATAAGCTGAC 126
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                                                                                                                     23;
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                                                                                   1 ATATAGAAGCCCAAGAAAAATCAGCTGAC 29
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                                                                                                                     Conservative
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                                                                                                                                      64.7%;
79.3%;
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                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                      Score 19.4; DB 9;
Pred. No. 2.7e+02;
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Pred. No. 5.2e+02;
0; Mismatches 4;
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                                                                                                                                2.7e+02;
                                                                                                                                                    Length 406;
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RESULT 12
US-10-027-632-147079/c
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CURRENT PAPPLICATION WINNERS: US/60218,006
PRIOR PAPPLICATION WINNERS: US/60218,006
PRIOR PAPPLICATION WINNERS: US/60/198,676
PRIOR PAPPLICATION WINNERS: US/60/199,676
PRIOR PAPPLICATION WINNERS: US/60/193,483
PRIOR PAPPLICATION WINNERS: US/60/193,483
PRIOR PAPPLICATION WINNERS: US/60/193,218
PRIOR PAPPLICATION WINNERS: US/60/185,218
PRIOR PAPPLICATION WINNERS: US/60/185,218
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                                           PRIOR PIPLICATION NUMBER: US 60/146,002
PRIOR FILTMS DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 355720
SOFTWARE: PasteSEQ for Windows Version 4.0
SEQ ID NO 147079
LEMSTH: 837
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GRHERAL HROSMATION:
APPLICANT: Wang, David G.
ITITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 147079
LENGTH: 837
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Best Local Similarity
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Publication No. US20030204075A9
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APPLICANT: Wang, David G.
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
ORGANISM: Human
                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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Pred. No. 3.
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                                                  CURRENT APPLICATION NUMBER: U8/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Charles, Boone
APPLICANT: Howard Bussey
TITES OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TLES REFERENCE: 10182-005-999
TLES REFERENCE: 10182-005-999
TURNER! PILING DATE: 2001-12-20
NUMBER OF SDQ ID MOS: 80010
SDGTMARE: Farentin version 3.1
SDGTMARE: Farentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6149, Application US/10032585 Publication No. US20030180953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6699, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                        NUPLICANT: Carr Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: X0, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Probaryotes
FILE REFERENCE: ELITA, 011A
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith 1
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n=g, a, t or c
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LOCATION: (408)..(408)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (408)..(408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1695
TYPE: DNA
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
APPLICATION NUMBER: 60/253,625
               APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                846 AGAACACCAAGAAAGATCAGCTGA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AGAMTCACAAGAAAAAACAGATGACC 55
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                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.2; DB 13;
Pred. No. 4.1e+02;
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
NUMBER OF SED ID NO: 14110
SOFTMARS: FASTSED for Windows Version 4.0
SED ID NO 6659
LENGTI: 2169
US-09-070-927A-292
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US-09-070-927A-292/c
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Patent No. US20020120116A1
GENERAL INFORMATION:
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                                                                                                                      INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,655

APPLICATION NUMBER: 65

APPLICATION NUMBER: 66/044,031

APPLICATION NUMBER: 66/046,031

APPLICATION NUMBER: 66/066,035

PILING DATE: 1997-11-14

ATTORNEY/ASSET INFORMATION:
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                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                SEQUENCE DESCRIPTION: SEQ ID NO: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GAAGCCCAAGAAAATCAGCTGAC 29
                                                         LENGTH: 20561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                   NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                     TELEFAX: (301) 309-8512
                                                                                                                                                                                          TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 4.3e+02
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Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
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                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to help are a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                           Score
     22
21.6
21.6
21.6
                                                                                                                                                     Query
Match Length DB
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     73.3
72.0
72.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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gb est: *
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454 12
477 10
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     BB035293
BM498025
BG266188
AI714933
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BE035293 MM05C05 M
BM498025 952032E05
BG266188 1000086G0
AI714933 606024G06
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20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20.2	20.4	20.4	20.4	20.4	20.6	20.6	21	21	21	21.2	21.4	21.6	21.6	۲
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476	465	461	461	458	444	428	416	415	415	388	387	381	371	365	348	322	309	301	301	288	286	282	281	239	209	1229	1317	778	570	498	730	344	700	692	411	664	940	649	645	559
10	10	14	9	10	N	ü	10	14	10	10	28	14	14	10	10	ö	10	ö	10	10	14	10	10	9	10	29	12	29	2	28	29	28	S S	5	13	28	29	11	ü	13
BF588622	BG150759	H53171	AW083647	180	3	308	ıχ	R19486		772	AZ831913	N73266			BF000738	BF060828	BF063598	BF063453	BB105699	BF063480	F07917	BF476962	BF476902	AV236858	BB324020	CC303312		CC081774	BI321439		BZ428389	BH761049	BH833230	BB048787	BU948624	AQ383884	CC304082	ĭ	487	BU049916
98	507	171	8364	06081	80963	BF060807	BE394869	R19486 y	BF060868	BF477200	AZ831913 2	N73266 y	R12015 y	BF001035	BF000738	BF060828	06359	BF063453	BB105699	BF063480	F07917 HS	BF476962	BF476902	AV236858	BB324020	CC303312	BI490262 6	CC081774	BI321439	A0254234	BZ428389	BH761049	вн833230	BB048787	4862	8388	œ	CT.	4487	BU049916
7110907.	nai02d05.	83	\mathfrak{L}	7127b04.x	Homo sapi	127a05.	$\ddot{\sim}$	1d06.r1	128g06.	taa64b09	M0111	v54h10.r1	1906.z	145g07.	143e07.	7127£09.x	7i23g11.x	7i24c06.x		7i24hll.	21E101	1aa56h09	naa55f08.	AV236858	3B324020	H261-59	50303207	350-K33r	saf11a05.	CpG0718A	BONEM78TF	BMBAC318G	BACPP4-B2	~		I11-J	ĕ	a mays	PP LEa002	1111017B0

ALIGNMENTS

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	COMMENT	TITLE	REFERENCE		SOURCE ORGANISM	DEFINITION ACCESSION VERSION	RESULT 1 BE035293/c LOCUS
University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, USA Fal: 520-621-7982 Fax: 520-621-7982 Fax: 520-621-690. Fax: 520-621	Contact: Michalowski, C.B.	H., Kawasaki, S., McCollough, A., Michalowski, C.B., Ralacio, C., Soara, G., Wheeler, M. and Zepeda, G.R. Eunctional Genomics of Plant Stress Tolerance	Dases 1 to 1086. 1 (Dases 1 to 1086.) Bohnert, H. J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Perrea	Sukaryota; Viridipilariae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridipilariae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Maddoctyledons; core eudicots; Caronhylllariae, Ajroseae, Macembryosthomm	EST. Mesembryanthemum crystallinum (common iceplant) Mesembryanthemum crystallinum	MM05CO5 MM Mesembryanthemum crystallinum cDNA 5', mRNA sequence. BE035293 BE035291.1 GI:8330205	BE035293 1086 bp mENA linear EST 07-JUN-2000

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JOURNAL
COMMENT
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM498025.1 GI:18649191
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                                                         (Promegal. cDNA was synthesized using both random and oligo(df) primers in separate reactions and equipped with BooRI adaptors. Library was size fractionated on aganose gels (for insert size y400b) and non-directionally cloned into RooRI-disected pUC19 vector. Blue/white selection on carbenticillin-containing places was used to recover positive clones.
                                                                                                                                                                                                                               /note="Vector: pUC13; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by deorge Rudenko using poly (A) selected RNA and Universal Ribocine cDNA Synthesis by (gromega). cDNA was synthesized using both random and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2032 row: E column: 05.
Location/Qualifiers
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/db_xref="taxon:3544"
/db_xref="taxon:3544"
/del_type="spidermal bladder cells"
/del_type="spidermal"
/del_type="spidermal bladder cells"
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db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Zea mays"
mol_type="mRNA"
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Pred. No. 7.1e+02;
0; Mismatches 5;
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102

TATAGAAGCCCAAGAGACCTCAGCTGGC 125 TATAGAAGCCCAAGAAAAATCAGCTGAC 29 24;

Conservative

72.0%;

Score 21.6; DB 10 Pred. No. 8.7e+02;

DB 10;

Length

477;

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Gaps

0

Mismatches

N

Zea mays Zea mays Bukaryota;

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

606024G06.x2 606 - Bar tissue mays CDNA, mRNA sequence. AI714933 AI714933.1 GI:5030739 EST.

AI714933

552 bp CDNA

mRNA linear BST library from Schmidt

EST 02-FEB-2000

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
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                                                                                                                                                                                                                                                                                                                      Email: walbot@stanford.edu
Plate: 1000086 row: G colu
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptopbyta, Embryophyta, Tracheophyta, Spemmatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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             /olone libe"1000 - Unique E from Maire Genome Project" (notee "This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maire genome project. Sequences are present from libraries 486, 487, 495, 603, 605, 606, 611, 618, 660, 687, 670, 707, and 945. Contigs were assembled using TIGN'S CAP program and a representative EST from each contig was elected for the Universe est. All singlets were also selected.
                                                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="mRNA"
/db_xref="dbEST:606024G06.x2"
      143 c
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                                                                        Email: walbot@stanford.edu
Plate: 1111017 row: B column: 02.
Location/Qualifiers
                                                                                                                                                                    Department of Biological Sciences Stanford University
                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogomeae; Zea.
                                                                                                                        Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                   855 California Ave, Palo Alto,
                                                                                                                                                                                                   Contact: Walbot V
                                                                                                                                                                                                                                   University
                                                                                                                                                                                                                                            Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                        Zea mays
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                    BU049916
                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA, mRNA sequence.
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855 California Ave, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                  Unpublished
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/organism="Zea mays"
/mol type="mRNA"
/db_xref="dbEST:952032E05.yl"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lab"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Organ: immature ear; Vector: pBK-CMV; Site 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue type="mixed"
(dey stage='ear length from 0.5 cm - 2.0 cm"
(lab bost="%LOLDE (Stratagene)"
(lab bost="%LOLDE (Stratagene)"
(lolne_lib="606 - Bar tissue cDNA library from Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:4577"
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(mol_type="mRNA"
(cultivar="Ohio43"
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85.7%;
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Pred. No. 8.9e+02;
D; Mismatches 4
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III from Maize Genome Project Zea mays
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                                                         Query Match
Best Local Similarity
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149
for the maize genome project, Sequences are present from library 952. Contigs were assembled using mmblascembler and 2 representatives from each contig were selected for the Unigene set. All singuist were also selected."

a 159 c 127 g 124 t
                                                                                                                                                                                                                           /dlone_lib="1111 - Uniquene_III from Maize Genome_Project. /note="This library represents the unique genes found in the third round of EST sequencing at Stanford University
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Query Match
          Local
  24;
          Similarity
 Conservative
         72.0%;
 0,
         Score 21.6; DB 13;
Pred. No. 8.9e+02;
 Mismatches
                 Length 559;
  Indels
 <u>.</u>
Gaps
 0
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152 TATAGAAGCCCAAGAGACCTCAGCTGGC 179 2 TATAGAAGCCCAAGAAAATCAGCTGAC 29

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DEFINITION
PP_LEGOZOMIOS Peach developing fruit mesocarp Prunus persica cDNA colone PP_LEGOZOMIOS, mRNA sequence.

BU044878
BU044878
BU044878
BU044878.1 GI:22484955
                                                                                          EST 26-AUG-2002
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RCE	Prunus persica (peach)
RGANISM	RGANISM Prunus persica
	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
	; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
ERENCE	1 (bases 1 to 645)
UTHORS	Callahan, A., Palmer, M., Main, D., Wing, R. and Abbott, A.

JOURNAL COMMENT Unpublished Peach Model Genome for Rosaceae

122 Long Hall, Clemson University, Clemson, SC 29634, USA Tel: 864 656 3060 Pax: 864 656 6879 Dept of Genetics and Biochemistry Clemson University Contact: Abbott, A.

Total High Quality bases = 603 Seq primer: TAATACGACTCACTATAGGG High quality sequence stop: 645. aalbert@clemson.edu Location/Qualifiers

source

/t.tsaue_type="Mesocarp"
//ab.boE=Ts_coli*
//ab.boE=Ts_coli*
//clone_lb="Peach developing fruit mesocarp"
//note="Westor: pBluescript II SK(-); Site_1: EcoRI,
//note="Westor: pBluescript II SK(-); Site_1: EcoRI,
//site_2: Modi, authority=Pennus persica L. Batch; The
sequence has been trimed to remove vector sequence a
contains a minimum of 100 bases of phred value 20 or
above: For move, decais on thiraty preparation and No. organism="Prunus persica" clone="PP_LEa0020M10f" db_xref="taxon:3760" cultivar="Loring" .645 type="mRNA"

and

189 sequence analysis go to
http://www.genome.clemson.edu/projects/peach. To order
this clone go to http://www.genome.clemson.edu/orders*
a 107 c 165 g 184 t

Matches 3 ATAGAAGCCCAAGAAAAATCAGCTGACC 30 72.0%; milarity 85.7%; Conservative 0; Mismatches Indels 0

Score 21.6; Fred. No. 9

DB 13;

Length 645;

Gaps

0

믕

ATTGAAGCCCAAGAAAATGCACCTGACC 108

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REFERENCE
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AY112254/c
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                                                                                                                                                                                                                                                                                                                            615 ATATAAGCCCAAGATAAATAAGCTGTCC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-ABE-2002) Maize Mapping Project, University of Missouri, Columbia, NO 6521, USA If you are interested in getting corresponding physical closes, these are publically available from EMBB and may be found by BLAST searching at MSI, maizemap.org; EMDB, www.mdb.iastrate.edu; TURR, www.ingr.org; or NOSE; www.indb.inm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford our pat Schnable, lows State, then clones may be requested from EmDB; www.mbb.iastrate.edu.
                                                                                                                                        genomic survey sequence
CC304082
CC304082.1 GI:30675523
                                                                                                                                                                                                      CC304082 940 by CH261-77A22_RM1.1 CH261 Gallus
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Zea mays
                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                          Gallus gallus
                                                                                              Gallus gallus (chicken)
                                                                                                                        GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
2 (bases 1 to 649)
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Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, SV.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enkaryota, Vizidiplantae, Streptophyta, Embryophyta, Txacheophyta, Spermatophyta, Magnoliophyta, Illiopsda, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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AY112254
AY112254.1 GI:21216844
HTC.
(bases 1 to 940)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes "this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed balont contigs; this resource was assembled by Dabont can part of a collaboration for to overgo addressing of Babs in conjunction with the Magping Project" 131 g 172 t 25 others
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/mol_type="mRNA"
/db_xref="MaizeDB:633041"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                Other GSSs: RPCII:-12217, TV
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Conter Dr., Rockville, MD
9712 Medical Conter Dr., Rockville, MD
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                                                                             Email: hloetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter be purchased from
(pieterselejoug med.buffalo.edu). Clones may be purchased from
BACPHC Resources (http://bacpac.med.buffalo.edu)corderib.
BACPHC Resources (info@respen.com) BAC end eserch page:
Research denetics (info@respen.com) BAC end eserch page:
http://www.tigr.org/udb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 664)
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Unpublished
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RPCI11-122J17.TJ RPCI-11
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Warren,W., Graves,T., Mardis,B. and Wilson,R.
Gallus gallus BAC End Reads
Unpublished
                                      Class: BAC ends
                                                                  Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Insert Length: 182000 Std Error: 0
Seq primer: RM1 TACGACTCACTATAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/close_lib="CH26!" inbred 256"
/close_lib="CH26!" inbred 256"
/close_lib="CH26!" inbred 256" incoxi; site_2: Ecoxi;
/note="Wester: pWREBAC2.1; Site_1: Ecoxi; site_2: Ecoxi;
/note="Wester: pWREBAC2.1; Site_1: Ecoxi; site_2: Ecoxi;
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Location/Qualifiers
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/mol_type="genomic_DNA"

/strain="Red_Jungle_Powl"
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95.7%;
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Pred. No. 1.
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Catarrhini;
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Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dmail: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University denome Sequencing Conter For information obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J (bases 1 to 411)
Melton D. Brown J. Kenty, G. Permutt A., Lee, C., Kaestner, K.,
Ismishka, I., Scearce, M., Brestelli, J., Gadavobi, G., Cliston, S.,
Hillier, L., Martan, M., Pape, D., Polio, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Riber, B., Roho, I., Semett, J., Cardenas
, M., Gibbons, M., McCann, R., Cole, R., Tagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MA 02138
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (hinoue@im.wustl.edu)
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Location/Qualifiers
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/ Choing. lib="MR95 isler" / Choing. lib="MR95 isler" / Mr95 - Mr95 / Mr
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/clone lib="RPCT-11"
/note="Vector: pBACe3.6; Site 1:
RPCIII Human Male BAC Libbrary"
113 c 111 g 166 t
                                                                                                                                                                                                                                                                                                     /tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127389"
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/mol_type="genomic DNA"
/db_xref="GDB:7546696"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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88.5%;
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Pred. No. 1.
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SOURCE

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77
School of Medicine, Box 8127, 660 South Euclid Ave., Louis, MC 63110, E-mail: hinoue@imgate.wustl.edu, Te 314-362-1916, Fax: 314-747-5692."

a 125 c 46 g 163 t
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BASE COUNT

Matches Query Match Best Local : 24; Similarity Conservative 70.0%; 0 Score 21; DB Pred. No. 1.4e 0; Mismatches DB 13; 1.4e+03; 13; Length 411 ű 0, Gaps

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369 2 TATAGAAGCCCAAGAAAATCAGCTGACC TATATAATCCTAAGGAAAAACAGCTGACC 30

묽 8

RESULT 11 BB048787/c POCOR.

DEFINITION BB048787 BB048787 BB048787 BB048787.2 GI:15404011 musculus cDNA clone RIKEN full-length enriched, 6430596G11 3', ğ mRNA sequence mRNA adult male olfactory bulb Mus linear EST 31-AUG-2001

SOURCE ACCESSION VERSION KEYWORDS Mus musculus EST Mus musculus (house mouse)

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Best

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

(Dasse 1 to 690)

Arakawa T. Caminoi, P., Fabida, S., Futmo, M., Hanagaki, T., Hara, A., Hitsanco, K., Hari, P., Tahia, Y., Ito, M., Kawai, J., Konno, H., Koulda, M., Kawai, O., Konno, H., Koulda, M., Kawai, O., Kawai, O

COMMENT JOURNAL.

Unpublished
On Jun 11, 2000 this sequence version replaced gi:8455935.
Contact: Yoshihide Hayashizaki

Labozatory for Genome Exploration Research Group, RIXEN Genomic Sciences Center (SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIXEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Jay
Tel: 81-45-503-9212 Kanagawa 230-0045, Japan

Bmall: genome-resege_criken.go.jp;
UKL:http://genome.gec.riken.go.jp;
Carninci.P., Shibatea,Y., Hayaten,N., Sugahara,Y., Shibatea,K., Itoh
(Karninci.P., Shibatea,Y., Hayaten,N., Sugahara,Y., Shibatea,K.,
M., Komno,H., Okazaki,Y., Muramatea,M. and Hayashisaki,Y.

Mormalization and subtraction of cap-trappe-selected CONNs to
prepare full-length cDNA, librarics for rapid discovery of new
genes. Genome Res. 10 (10), 1517-1530 (2000)

wasji,K., Pulyatea,S., Touce,K., Togawa,Y., Izawa,M., Ohara,E.,
Washi,J.W., Okazaki,Y., Maramatelu,M., Touce,J., Kiza,A. and

Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system-384-format esquencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Conno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara

Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA encyclopedia real-time sequence clustering for construction of a mouredundant cDNA library, Genome Res. 11(2), 281-289 (2001) Yamanaka, I. K. Mayosawa H. Kondo, S. Sasko T. Shibagawa A., Alzawa K. R. Pikuda S. Hara, A. Itoh, M., Kawai, J., Shibata, K., Arakawa, T. rehit, Y. and Hayashiraki, T. Toh, M., Kawai, J., Shibata, K., Arakawa, T., Rapping of 19012 muse cDNAs on mouse Chromosomes. J. Struct. Puts. Genomics 2 prep LT2-186 (2001) The Computer of the Compute further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

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VERSION
KEYWORDS
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BH833230
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                                                                                                                                                                                                               AUTHORS
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                                 Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371
                                                                                                                                                    Srinivasan, J. Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Rav, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A., Jes
Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J.
A. BRC-based genetic linkage map of the nematode Pristionchus
Email: ralf.sommer@tuebingen.mpg.de
                                                                                       Evolutionary Biology
                                                                                                     Contact: Sommer RJ
                                                                                                                        Unpublished
                                                                                                                                      paci
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                 Pristionchus pacificus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      olfactory bulb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="olfactory brain"
/dev_stage="adult"
/lab_host="DH10B"
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|strain="C57BL/6J"
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Pred. No. 1.5e+03;
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8

ORIGIN

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COMMENT

Query Match

68.7%;

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RESULT 13
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Best Local Similarity
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BMBAC318G10T7 PSU Brugia malayi G
genomic, genomic survey sequence.
BH761049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
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Onchocercidae; Brugia.

1 (bases 1 to 344)

Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N.,

Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N.,

J., Guiliano,D., Slatko,B. and Blaxter,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brugia malayi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: T7 (TAMTACGACTCACTATAGGG) Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome survey sequences from the human parasitic nematode Brugia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196
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           ρ
/dev_neiges_mitroffilaris_(ii)"
/dev_neiges_mitroffilaris_(ii)
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170 c 150 g 184 t
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/mol_type="genomic DNA"

/strain="var. California"

/db_xref="taxon:54126"
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="genomic DNA"
strain="TRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Brugia malayi"
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Pred. No. 1.5e+03;
0; Mismatches !
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Best Local

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REFERENCE
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                                                                                          REFERENCE
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ORGANISM
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VERSION
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                                 TITLE
                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whole genome shotgun sequencing of Brassica oleracea Unpublished other_GSSs: BONEM78TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EX428389 DNA linear GS 13-050 DNA linear GS 13-050-200 BOREM78TF BO 1.6.2 KB tot Brassica oleracea genomic clone BONEM78 genomic survey sequence.
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BZ428389.1 GI:26671205
GSS.
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                                                                                                                                                                                                                                                                                                                                                           AQ254234 498 bp DNA linear (CpG0718A CpIOWAgDNA1 Cryptosporidium parvum genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bmail: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea
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Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis
                                                                                                                  Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida, Cryptosporidiidae, Cryptosporidium.
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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Pred. No. 2.2e+03;
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                                   1 ATATAGAAGCCCAAGAAAAATCAGCTGACC 30
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Tel: 415 206 8846
Fax: 415 206 3353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Depts. of Medicine & Pharmaceutical Chemistry San Francisco General Hospital-University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nelson, R. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
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                                                                                                               Similarity
ATAAAGAAATTCAAGAAAATCTGCAGACC 466
                                                                                                                                                                                                            222
                                                                                         Conservative
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Calome lib="portowagnMa;

Apparum (TOMA isolate) genomic DNA was hydrodynamically asserted to produce fragments having a tight size of the first produce fragments having a tight size of the first produce fragments having a tight size of the first produce fragments having a tight size of the first produce fragments having a tight size of the first produce fragments having a tight size of the first produce fragment of the produce have sent produced fragments and DNA sephacry; 6-400 to remove any small fragments and DNA eleting in the roid volume was subcloned into an EcoR v.digested, alkaline phosphates-tracted phlueScript II (SK) vector and transformed into E coil strain XLZ Blue MRF. Recombinant clones from the first planing of the MRF, where selected for sequence analysis using 31 and animally were selected for sequence analysis using 32 and
                                                                                                                                                                                                                              T7 primers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Cryptosporidium parvum"
/mo1 type="genomic DNA"
/strain="10WA"
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                                                                                                               Score 20.4; DB 28
Pred. No. 2.4e+03;
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                                                                                         Mismatches
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model Run on: December 18, 2003, 09:02:7, Search time 1143.11 Seconds (Without alignments) 913.763 Willion cell updates/sec

Title: Perfect score: Sequence: US-09-889-491-13 30

Scoring table: Gapop 10.0 , Gapext 1.0 1 atatagaagcccaagaaaaatcagctgacc 30

2888711 seqs, 20454813386 residues

Searched:

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:* gb_pat*
gb_ph:
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gb htg:*
gb in:*
gb om:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	c 45	C 44	c 43			c 40	39		c 37	36	c 35		33	o 32					27	26		c 24	23		21							13	12	Ľ	c 10		ດ ດ ໝ ຈ		אנ	ла	۱ ۵		, _p	-	Result
	20.4	20.4	20.4	20.4	20.4	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.8	20.8	21	21	21	21	.21	21	21.2	21.2	21.4	21.4	21.6	21.0	21.0	21.6	22.2	22.2	22.2	22.2	22.2	200	22.2	3 6	200	3 6	20.00	3	30		Score
	68.0	68.0	68.0		68.0	68.7	68.7	68.7	68.7	68.7	68.7	68.7	68.7	68.7	69.3	69.3	70.0	70.0	70.0	70.0	70.0	70.0	70.7	70.7	71.3	71.3	71.0	3.0	72.0	•	74.0	4	74.0	74.0	74.0		74.0	3:	77.		20.	70.0			Query
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	AC135427 Ox	Z81121 Caer	M95725 Gall	AX251443 Se	AX654979 Se	AC097832 Ra		AC136662 Ra		AC117999 Mg		AL161666 Ht				AC096644 Hc		AC010932 Hc	BX248103 Da	AL929590 Ze	AL133510 Hu				AC114851 Ra		ACIZ6342 HO						AC087856 Ho		AL354862 Hu		AX695617 Se		ACCOUNT NO			10110663 Ba			Description
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ALIGNMENTS

LOCUS DEFINITI ACCESSIO VERSION KEYWORDS SOURCE ORGANI REFERENC RUTHOR TITLE JOURNA		7
LOCUS AXO28510 DEFINITION Sequence 13 from Patent WOO04216. ACCESSION AXO28510 URRINON AXO28510. GIANOPORT HONOR AND HONOR HON	AX028510	RESULT 1

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REFERENCE
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KEYWORDS
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AUTHORS
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HUMBNSP01
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Rattus norvegious
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                                                                                                                                             Rattus norvegicus clone CH230-83K21,
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                Rattus.
                       Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                   AC110652.5 GI:25100613
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                                                                                                                               unordered pieces.
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Matrix Biol. 14 (1), 31-40 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metasoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 2415)
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L24756.1 GI;4
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(bases 1 to 222706)
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ilarity 100.0%; Pred. No. 0.075;
Conservative 0; Mismatches
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437 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                       gene="BNSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="Unassigned"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Pred. No. 0.06;
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(BNSP) gene, exon 1.
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                                                                                                                             COMMENT
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AUTHORS Manual V. Malie M. Marchet, Auguston, S. Manns, C., Algorian, C., Manns, C., Chen, Y., Chen, Z., Chi, J., Charles, C., Daves, D., Chan, G., Chen, R., Chen, Y., Chen, Z., Chi, J., Claveland, C., Deanen, S., Daman, C., Ding, Y., Dinh, H., Divya, K., Dagar, R., Danns, C., Ding, Y., Dinh, H., Divya, K., Dagar, H., Dayer, H., Dagar, R., Dagar, C., Ding, Y., Dinh, H., Divya, K., Dagar, R., Dagar, C., Ding, Y., Dinh, H., Divya, K., Dagar, H., Dagar, R., Dagar, C., Ding, Y., Dinh, H., Divya, K., Dagar, H., Dagar, R., Dagar, C., Ding, Y., Dinh, H., Divya, K., Dagar, H., Dagar, R., Dagar, C., Ding, Y., Dinh, H., Divya, K., Dagar, H., Dagar, R., Dagar, R., Dagar, C., Ding, Y., Dinh, H., Divya, K., Dagar, H., Dagar, R., Martia, Submitted (14-FBE-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 1 (Dases I to 222706) Direct Submission Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Unpublished (bases 1 to 222706)

TITLE
JOURNAL
REFERENCE
AUTHORS REFERENCE TITLE JOURNAL JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Direct Submission Rat Genome Sequencing Consortium.

of Molecular and thuman Genetics Baylor College of Medicine, Ome Baylor Plaza, Houston, T77030, USA Of Nov 19, 2002 this sequence version replaced gir23101016. The sequence in this assembly is a combination of BAC based reads and whole genome shotgum sequencing reads assembled using Atlas (http://www.lage.bom.tmc.edu/projecte/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-casffold'). Within sach contig-casffold assembly (a 'contig-casffold'). Within sach cortis-casffold and optanted, and separated by streed paps filled with Ms to the serianted size. The sequence contigs within a contig-casffold that continue that the contigue that the contigue that the contigue the contigue that the contigue the contigue that the contigue that the contigue that the contigue the contigue that the contigue that

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                                                                                                                                 HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AC096147.6
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235996 bp DNA linear HTG 10-PRAFT SEQUENCE CH230-10H14, WORKING DRAFT SEQUENCE
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                                                       Kattus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Betimated insert size may differ from sequence length (see http://www.lgsc.hom.tmo.edu/docs/dechank_draft_data.htmose).

NOTE: This is a warking draft sequence. It outsets!)

consists of contigs. The true order of the places is not known and their order in this sequence second is arbitrary (see herwest the contigs are represented as arbitrary cape between the contigs are represented as arbitrary cape herwest the contigs are represented as arbitrary cape herwest the contigs are represented as arbitrary cape herwest the contigs are represented as a runs of N. but the exact sizes of the cape are unknown.

This record will be updated with the finished sequence.
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Center project name: GSPZ
Center clone name: GSPZ-183Z1
Center clone name: GSPZ-183Z1
Assembly program Phrap; version 0.990329
Consensus quality: 214884 bases at least 030
Consensus quality: 214894 bases at least 030
Consensus quality: 218205 bases at least 020
setimated linear taze: 2215899 sem-o-contigs
setimated finear
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/clone="CH230-83K21"
complement (195782...196630)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="clone_boundary
clone_end:Sp6
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44575 c 46422 g 62
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18001: gap of unknown length
127149: contig of 199140 bp in length
217249: gap of unknown length
221403: contig of 4154 bp in length
221503: gap of unknown length
221503: gap of 1203 bp in length.
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SOURCE

VERSION

Focus

COMMENT

REFERBNCE AUTHORS TITLE

JOURNAL

JOURNAL

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prejach (Ducan Books S. Duch) A. Duchin K. Hurch B. Reves K. Eggan A. Becotto M. Soggan, G. Brang C. A. Table T. Fan G. C. F. Fraser, C. M., Rocker, P. Fraser, C. M., Gabisi, A. Gabisi, A. Garcia, M. Gabrer, M. Rocker, P. Fraser, C. M., Gabisi, A. Gabrer, C. Garcia, M. Gabrer, G. Garcia, M. Marcia, M. Mar to Submitted (10:48X-2003) Human Genome Sequencing Center, Department to Molecular and Human Genetics and Suprior College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:4481820.
The sequence in this assembly is a combination of BaC based reads and whole genome shoragm sequenciny reads assembled using Atlas (http://www.hggc.bem.tmc.edu/projecte/rat/). Each contig described in the feature thale balow represents a conficial in the Atlas assembly (a 'contig-scaffold'), Within each contig-scaffold in the Atlas assembly (a 'contig-scaffold'), Within each contisted and separated by sized gaps filled with Ms to the estimated size. The sequence may extend beyond the ends of the Jone and thore may be sequence contigs and thin a contig-scaffold that consist entirely of whole genome shought separated reads. Both come and thore may be sequence contigs within a contig-scaffold that consist entirely of whole genome shough separated reads. Both ends sequences and whole genome Auyalebechi, V., Aoyagi, A., Ayodeji, M., Bada, E., Badeh, M., Benahmed, F., Balderin, D., Bandarmanike, D., Barber, M., Barnstead, M., Benahmed, F., Bisea, D., K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, M., Blayart, M., Barkenburg, K., Blyant, M., Barnstead, M., Carteron, M., Bryant, M., Carteron, M., Carteron, M., Carteron, M., Carteron, M., Carteron, C., C Direct Submission
Direct Submitted (17-SEP-2001) Human Genome Second Molecular and Human Genetics, Baylor Plaza, Houston, TX 77030, USA Unpublished Allen, C., Allen, H., Alsbrooks, S., Direct Submission Rat Genome Sequencing Consortium. Direct Submission (bases 1 to 235996) (bases 1 to 235996) Amin, A., Anguiano, D Sequencing Center, Department lor College of Medicine, One Benahmed, F.,

TITLE JOURNAL REFERENCE AUTHORS

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ACCESSION
VERSION
                                                                                                         DEFINITION
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                                                            Rattus norvegicus clone CH230-304Kl2, ***, 8 unordered pieces.
Rattus norvegicus (Norway rat)
          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                          ACI31002
ACI31002.2 GI:23195369
                                                                                                                                                                                                                                                                                      1 ATATAGAAGCCCAAGAAAAATCAGCTG 27
                                                                                                                                                                                                                                                                                                                                    25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is beliaved to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
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Center Loren amer: GERN
Center Core name: GERN-10114
Center Core name: GERN-10114
Center Core name: GERN-10114
Center Core name: GERN-10114
Consensus quality: 22450 bases at least Q40
Consensus quality: 22450 bases at least Q40
Consensus quality: 225657 bases at least Q40
Consensus quality: 228657 bases at least Q40
Retimated Linear date: 3270857 num-c-comities estimation
Retimated Linear date: 3270857 num-c-comities estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the finished sequence as soon as it is available and
e accession number will be preserved.

1 235996: contig of 235996 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                           end_sequence:BH305686"
47400 c 49017 g 66511 t
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site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end_sequence:BH305688"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (231640. .232490)
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clone_end:Sp6"
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|db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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Pred. No. 1:
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                                                                                                                               DNA
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SEQUENCING IN PROGRESS
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SOURCE

COMMENT

of Molecular and Human Genetics; Baylor College of Medicine, One Baylor place, Houston, TY 7020, Uts On sep 19, 2002 this sequence version replaced gi-2267833, On sep 19, 2002 this sequence version replaced gi-2267833 The sequence in this secondry is a combination of BMC based reads and whole genome shortpun sequencing reads assembled using Atlas and whole genome incendifyprojects/rat/). Each contig described in the feature table below represents a scaffold in the Atlast between the feature table below represents a scaffold in the Atlast between the control of the contr

Submitted (08-OCT-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine,

Department

REFERENCE

of Molecular and Human Genetics, Baylor Plaza, Houston, TX 77030, 3 (bases 1 to 266204)

Submitted (16-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Flaza, Houston, TX 77030, USA

AUTHORS

JOURNAL

Direct Submission

Rat Genome Sequencing Consortium.

AUTHORS

Direct Submission

2 (bases 1 to 266204)
Rat Genome Sequencing Consortium

JOURNAI

TITLE JOURNAL REFERENCE REFERENCE AUTHORS ORGANISM Alley C. Walter, H. Walter, H. Walter, H. Walter, H. Walter, W. Walter, H. Wa Rattus norvegicus Eukaryota; Metazoa; Mammalia; Eutheria; Unpublished Direct Submission Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., (bases 1 to 266204) Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Adams, C Alder, J.,

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BASE COUNT
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(see http://www.hgsc.bom.tmc.edu/docs/ecbabh/draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This sequence may represent more than one clone.
NOTE: This sequence may represent more than one clone.
NOTE: This sequence may represent one clone.
NOTE: This sequence represented as arbitrary. Gaps between the coming are represented as arbitrary. Gaps between the coming are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession mumber will
         74833
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Center project name: CH203-304X2

Center clome name: CH203-304X2

Assembly program: Phrap, version 0.990329

Consensus quality: 441340 bases at least 0.00

Consensus quality: 44135 bases at least 0.00

Consensus quality: 447564 bases at least 0.00

Gonsensus quality: 447564 bases at least 0.00

Stimated hisert size: 263831 sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; man-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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                                                                                                                             /note="wgs_contig"
97500. .99312
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102208. .104470
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50743 c 51682 g
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104571. .106534
                                                                                                                                                                                                                                                                              /db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
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259811 contid of 1054 bp in lensth
259811 gap of unknown length
260123 contid of 1242 bp in lensth
260123 contid of 1242 bp in length
260233 gap of unknown length
261399 contid of 1350 bp in length
261399 gap of unknown length
261391 gap of unknown length
262961 gap of unknown length
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256510: gap of unknown length
257627: contig of 1117 bp in length
                                                                                                                                                                                                                                                                                                                                                  type="genomic DNA"
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    72374 t 16572 others
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AC004810
86491 bp DNA linear PRI 13-OCT-1:
Homo mapiens chromosome Y, clone hCIT.69_H_8, complete sequence.
                                 AC004810
AC004810.1 GI:3264567
                                                                                            PRI 13-OCT-1999
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ACOU4810 밁

87745 ACATAGAAGCCCATGAAAAATCAGCTG 87771

VERSION

KEYWORDS ACCESSION DEFINITION POCOS.

SOURCE ORGANISM Homo sapiens Homo sapiens (human)

REFERENCE AUTHORS REFERENCE JOURNAL Bukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butberda, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 86491, Linton,L., Nusbaum,C., Page,D. and Lander,E Birren,B., Rasman,K., Linton,L., Nusbaum,C., Page,D. and Lander,E Homo, septems Chromosome Y, Clone hCTT.65_H.8 unpublished Page, D. and Lander, E.

AUTHORS TITLE

Birrin, B., Fement, K., Lintcon, L., Musbaum, C., Lander, S., Allen, M.,
Belker, J., Baldwin, J., Berna, M., Beckerly, R., Benn, J., Beshin, C.,
Beutwell, C., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, B.,
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Peterson, K., Riley, R., Soberts, D., Rossello, R., Roy, A., Shyam, R.,
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P., Marken, A., Mangle, B., Meesler, J., Baller, J., Shur, C.,
P., M., Wessiller, A., Mangle, B., Meesler, J., Baller, J., Baller, J., Borne, C.,
P., Marken, A., Mangle, B., Meesler, J., Baller, J., (bases 1 to 86491)

REFERENCE JOURNAL AUTHORS

Direct Submission

the Submitted (Obc-UNM-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

32 (bases 1 to 86491)

33 (bases 1 to 86491)

34 Shren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, M., Baker, J., Baddwin, J., Barna, M., Beckerly, Benn, J., Beatin, C., Boutwell, C., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, E., Bevon, K., Dewar, K., Doolan, J., Esemadi, S., Perreita, P., Depayre, E., Bevon, K., Dewar, K., Doolan, J., Esemadi, S., Geraige, D., Gardyna, S., Strikhigh, W., Forzest, C., Fuñce, R., Gage, D., Gardyna, S., Strikhigh, W., Forzest, C., Fuñce, R., Gage, D., Gardyna, S., Strikhigh, W., Forzest, C., Fuñce, R., Gage, D., Gardyna, S., Harris, K., Horton, I., Houland, J., C., Hil, L., Jacobe, L., Kam, J., Machian, M., McKlenn, P., McGurk, M., McKerna, K., McKenn, E., McCarb, P., McCurk, M., McKerna, K., McKenna, K., McKenna, C., Bevlin, B., McKens, C., Bevlin, B., Peterson, K., Rider, R., Roberts, D., Rossello, N., Boo, A., Shyam, R., Strickkand, C., Subramanian, A., Torriella-Hiller, W., Scone, C., Washisty, H., Strickkand, C., Subramanian, A., Torriella-Hiller, Y., Se, M.J., Mao, J., and Yon, A., Washisty, H., Stone, C., Strickkand, C., Subramanian, B., Strick, B., McCense, C., Ph., V., Le, M.J., Mao, J., and Yon, A., Washisty, B., McCense, J., Ph., Y., Le, M.J., Mao, J., and Yon, A., Washisty, H., Stone, J., Washisty, H., Stone, J., Washisty, H., Yon, M., Washisty, H., Washisty, M., Washisty, M and

Direct Submission

REFERENCE

AUTHORS JOURNAL

ut Sübmitted (727-UNM-1998) Whitehead Institute/MIT Center for Genome Research, 220 charles Street, Combridge, MA 02141, USB.

4 (Bases t. to 86.92)

4 (Bases t. to 86.92)

5 (Bases t. to 86.92)

6 (Bases t Direct Submission Vo,A., Wagner,A., Wang,B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and

1 ATATAGAAGCCCAAGAAAAATCAGCTG 27

Query Match Best Local Similarity Matches 25; Conser

79.3%; ilarity 92.6%; Conservative

; Score 23.8; I ; Pred. No. 19; 0; Mismatches Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-00T-1999) Whitehead Institute/MIT Center for Genome Research, 220 (Charles Street, Cambridge, MA 02141, USA On Jun 27, 1996 this sequence version replaced gi:2233125.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, F. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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/rpt_family="MSTA"
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                                                                                                                      complement (6801. .7104)
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lement(4181. .4585)
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RESULT 7 AC120085/G AC120085 LOCUS AC120085 DEFINITION Rattus no	Qy 2 TATAGAAGCC Db 44376 TATAGAAGGC	Query Match Best Local Similarity Matches 25; Conser	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		879	repeat_region	repeat_region		STS	. repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		STS	repeat_region	repeat_region	STS
195296 bp DNA 195296 bp DNA ***	TATAGAAGCCCAAGAAAATCAGCTGAC 29 	77.3%; Score 23.2; DB 9; L 89.3%; Pred. No. 36; vative 0; Mismatches 3;	complement (15972 16220)	complement (15833. 11565)	/ tyc_ramity="Atta:" complement (15653, 15831) /ror family="MRDM (pre-mal"	001101	/TDC ramily="Alusg" complement (1493115353) /TDT family="MUDDA intownol"	14617. 14912 14617. 14912	complement; 14305 14587)	complement (14200. 14279) /rot family="MRR4 internal"	13989. 14199 /rot family="TRR8"	complement (13486 13986)	complement (12967 13508)	complement (1265912966) /rot family="Aluso"	/note="acc: number AA204659, match to zc81b05.rl"	1146211556	complement (11441 12658) /rpt_family="MBR4_internal"	1114711432 /rpt family="Aluy"	/Botaluard indine="Bor" /note="acc. number AA204659, match to zg81b05.rl"	10560. 10604	<pre>complement(1023311146) /rpt family="MER4 internal"</pre>	complement (1007610213) /rpt family="MER4A2"		9528. 9762 9528. 9762 /rpt family="MER4A"	9038. 9314 /rot family="All:Jos	8858. 8960 /rpt family="Aludb"	/standard name="EST" /note="acc. number AA207105, match to	86829075		8408, 8517	8147, .8524 /standard_name="EST" /note="acc. number AA224051, match to
linear HTG 12-OCT-2002 SEQUENCING IN PROGRESS		ength 86491; Indels 0; Gaps 0;													o gi 1802573, clone				o gi 1802573, clone								o gi 1802456, clone		•		o gi 1844592, clone

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Submitted (12-0CT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                           Submitted (03-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetice, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                        Direct Submission
                                                                                                               Rat Genome Sequencing Consortium
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-seaffold that consist entirely of whole genome shotgum sequence reads. Both end sequences and whole genome On Oct 12, 2002 this sequence version replaced gi:21/7/200.
The sequence in this assembly is a combination of BMC based reads
and whole genome shortgun sequencing reads assembled using Ralas
(http://www.hgc.bmt.tnc.ed/projecter/arx/). Each counting decorabed
in this feature table below represents a scaffold in the Atlas
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig'-carfold'). Within ach (contig'-scaffold, shotgun sequence only contigs will be indicated in the feature Genome Center

(see http://www.hgsc.bom.tuc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and thair order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence NOTE: Estimated insert size may differ from sequence length be preserved as soon as it is available and the accession number will Center project name: GW20-46088
Center clone name: GW20-46088
Resembly program: Phrap; version 0.990329
Consensus quality: 17555 bases at least 0.00
Consensus quality: 17555 bases at least 0.00
Consensus quality: 17855 bases at least 0.00
Consensus quality: 180615 bases at least 0.00
Destinated insert size: 177042 bases at least 0.00
Bathanted insert size: 177042 bases at least 0.00
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Datinated Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Project Information Center: Baylor College of Medicine Center code: BCM /note="wgs_end_extension clone_end:Sp6" /note="wgs_end_extension clone_end:Sp6" 179471 .180564 clone_end:Sp6 site:MboI end_sequence:RXBRP04TJ" complement(167606. .168 5152. /note="wgs_end_extension clone_end:T7" 173865 .177056 gite:MboI note="clone_boundary lone_end:T7 /mol_type="genomic DNA" /db_xref="taxon:10116" organism="Rattus norvegicus" note="clone boundary 'clone="CH230-490B8" 184779; contig of 184779 bp in length
184879; spp of unknown length
188094; contig of 3215 bp in length
188194; spp of unknown length
191782; contig of 3586 % in length
191882; contig of 3586 % in length
191882; contig of unknown length
192300; contig of 1318 bp in length
193300; contig of 1358 bp in length. .195296 .1322 sequence: RXBRP04TV" .6277 'Qualifiers .168692)

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REFERENCE
AUTHORS
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      Direct Submission
Unpublished
2 (bases 1 to 139
                                                              Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Enteleogromi, Mammalla, Butheria, Primates, Catrithin, Monindes, Homo. et al. (Dases 1 to 19973)
DOB Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                        3 ATAGAAGCCCAAGAAAATCAGCTGAC 29
                                                                                                                                        Homo sapiens
                                                                                                                                                           Homo sapiens (human)
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HTG.
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                                                                                                                                                                                                                                         Homo sapiens chromosome 5 clone CTB-91024, complete sequence.
                                                                                                                                                                                                                                                            AC010612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel compositions and methods for cancer patent: WO 03008583-A 1244 30-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morris,D.W. and Engelhard, E.K.
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AX695617
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clone_end:Sp6"
a 41149 c 42292 g 48361 t
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/db_xref="taxon:9606"
, 20559 c 21158 g 26915 t
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/note="wgs_end_extension
clone_end:Sp6"
188195. .189223
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clone_end:Sp6"
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clone_end:Sp6"
182511. .184779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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Pred. No. 9
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Pred. No. 3
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AL Submitted (16:NOV-2001) Wellcome Trust Sanger Institute, Hinton, cabbilities (16:NOV-2001) Hellcome Trust Sanger Institute, Hinton, cabbility Cable (16:Nov-2001) Hellcome requests: clonerequest@sanger.ac.uk on Oct 29:201 this sequence version replaced giisSilli3. During sequence assembly data is compared from overlapping clones. Where differences are found these are amoutated as variations together with a note of the overlapping clone, as we submit sequences with variation mortation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 301); an attempt was made to response all sequencing problems, such as compressions and repeate; all regions were covered by at least one plasmid abbclume or nore than one Mis subolume; and the seembly was confirmed by restriction digest: The following above abbreviations are used to associate primary accession numbers given
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Garner, P

(bases 1 to 153954)

Direct Submission

HIG

GI:16508203

Homo sapiens AL354862.11 sequence.

Homo sapiens (human)

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; AL354862 153954 l Human DNA sequence from clone

153954 bp DNA linear Pom clone RP11-83L6 on chromosome

PRI 16-NOV-2001

complete

ACAGGAGCCCAAGAAAATCTGCTGAC 39693

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Local Similarity
3 ATAGAAGCCCAAGAAAAATCAGCTGAC 29
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Direct Submitted (14-SEP-1999) Production Sequencing Pacility, DOB Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 (16ases 1 to 119878)

DOB Joint Genome Institute and Stanford Human Genome Center.
                                               24;
                                                                                                                                                                                                                                                                                                                                                                      Quality: Phrap Quality >=40 99.6% of Sequence
Estimated Total Number of Errors is 0.4.
                                                                                                                                                                                                                                                                                                                                                                                                              www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-JUL-2001) DOS Joint Genome Institute, 2800 Mitchell 
Drive, Walnut Creek, Ch 94598, UGA
On Jul 20, 2001 this sequence version replaced gi:14277265.
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DOS Joint Genome Institute and Stanford Human Genome Center
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Submitted (01-4)WY-2001) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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                                                                                                                                                                         39291
                                               Conservative
                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                     /clone="CTB-91C24"
31188 c 29449 g 39945
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                        chromosome="5"
                                                                   88.9%;
                                                                                              74.0%;
                                               9
                                                                      Score 22.2;
Pred. No. 94;
                                               Mismatches
                                                                                                  DB 9;
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                                                                                              Length 139873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71403 ACAGGAGCCCAAGAAAATCTGCTGAC 71377
Submitted (25-AUG-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                           Bruno, D., Conn, L., Dela Rosa, M., Glukhov, S., Hansen, N., Hyman, R., Ramirez, D. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the feature table with their source databases: IM:, MMILI, SW:, SWISSEROY, ET., TERMEL, Mp., WORMEEP, Information on the WORMEEP bitsp.//MWW.asinger.ac.uk/Frojects/C_elegans/wormep This sequence was generated from part of bacterial clone contige of human chromosome 9 constructed by the Sanger Centre Chromosome 9 Mapping Group, Burther information can be found at high-ly/www.sanger.ac.uk/HGE/Chry SWIJ-3156 is from the library RGCT-11.1 constructed by the group of lates de Jong. For further details see
                                                               Direct Submission
                                                                                                                                                                                                                         Bruno,D., Coun,L., Dela Rosa,M., Federspiel,N., Foreman,P.,
Glukhov,S., Hansen,M., Hyman,R., Meo,J., Maratho,R.,
Morehouse,A.J., Oefiner,P., Falm,C.J., Ramirez,D., Wilhelmy,J.
                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome
AC009514
                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC009514.2 GI:6016667
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                                                                                                                                                                                                                                                                                                                                                                                                           flomo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 74.0%;
Similarity 88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGAAGCCCAAGAAAAATCAGCTGAC 29
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                                                                                                                                                                                                         and Davis, R.W.
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40170. 40389
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/note="Sequence from overlapping clone RF11-148I22
(AL162585). Assembly confirmed by restriction digest."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11.1"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ne 8 clone RP11-4K16,
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Pred. No. 93;
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                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                              Pederspiel, N., Foreman, P.,
Mao, J., Morehouse, A.J., Oefner, P.,
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REFERENCE

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ACCESSION

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Biren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC087856.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 8, clone RP11-4K16, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-NOV-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morshouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu.S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-OCT-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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Glukbov, S., Handen, N., Hyman, R., Mao, J., Marathe, R.,
Morebouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J.,
                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 8, clone RP11-4K16
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/clone_lib="R human BAC library 11"
33519 c 32897 g 53557 t
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ORIGIN

/Tpt family="THEIB"
complement(1171. .1606)
/Tpt family="MLTIC"
1732. .1803

2. .304 /rpt_family="THELB"

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clone_ThP11-4K16" clone_Thb="RPCI-11 Human Male BAC"	. 9000	sapiens" NC DNA"	iers	4_K_16	Project Information ect name: L12361	Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu	stitute/ MIT Center for Genome Research	<pre>""""""""""""""""""""""""""""""""""""</pre>	(1996-1997)	On Dec 19, 2002 thise squence version replaced gi:24796931.	Whitehead Institute/MIT Center for Genome	oun, J., Zembek, L., Zimmer, A. and Zody, M.	<pre>ith,C., Spencer,B., Stange-Thomann,N., Tesfaye,S., Theodore,J., Topham,K.,</pre>	., Plerre, N., Raymond, C., Retta, R.,	ylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Donnell,P., O'Neil,D., Oliver,J.,	<pre>MacLean, C., Macdonald, P., Major, J., Meldrim, J., Meneus, L., Mihova, T.,</pre>	ne, W., Iliev, I., Johnson, R., Jones, C., 11s, C., Landers, T., Levine, R.,	<pre>tzGerald,M., Gage,D., Galagan,J., ham,L., Grand-Pierre,N., Hafez,N.,</pre>	llano,K., Dewar,K., Diaz,J.S., Dodge,S.,	<pre>RS Birren, B., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,</pre>	reet, Cambridge, MA 02141, USA	Whitehead Institute/MIT Center for Genome	<pre>oun,J., Zembek,L., Zimmer,A. and Zody,M.</pre>	<pre>ith,C., Spencer,B., Stange-Thomann,N., Tesfaye,S., Theodore,J., Topham,K.,</pre>	., Pierre, N., Raymond, C., Retta, R., J., Roy, A., Schauer, S., Schupback, R.,	ylor,J., Nguyen,C., Nicol,R., Norbu,C., , O'Donnell,P., O'Neil,D., Oliver,J.,	MacLean, C., Macdonald, P., Major, J., Meldrim, J., Meneus, L., Mihova, T.,	lme, W., Iliev, I., Johnson, R., Jones, C.,	<pre>itzGerald,M., Gage,D., Galagan,J., iham,L., Grand-Pierre,N., Hafez,N.,</pre>	<pre>hazaro,B., Choepel,Y., Collymore,A., hlano,K., Dewar,K., Diaz,J.S., Dodge,S.,</pre>	Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,	320 Charles Street, Cambridge, MA 02141, USA 1 to 169060)	Whitehead Institute/MIT Center for Genome	Wilson, B., Wu, X., Myman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	<pre>\rangle A., Talamas, J., Testaye, S., Theodore, J., \text{Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,} \]</pre>	
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REFERENCE
AUTHORS
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AUTHORS
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Submitted (16-7AM-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (16-84) (Charles Street, Cambridge, MA 02141, USA (16-84) (Charles I to 181607) (Charles I, Alian, Allen, M. Birran, B. Lilfon, L. Musbaum, C., Lander, E., Alian, Allen, M. Bastian, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarta, V., Camarta, V., Charro, B., Charles, V., Charl
                                                                                                                                                                                                                                                                                                                                                                                                      Zimmer, A. and Zody, M. Direct Submission
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases l to 181607)
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complement (40131. ...
/rpt_family="MER94"
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submitting the middle 181607 bps of the clone [111208 = unique]

and AC021582 (WICGR project L5758) at the T7 end by 81850 bps. We

overlaps AC021580 (WICGR project 15756) at the SP6 end by

Web site: http://www-seg.wi.mit.edu
Contact: sequence submissionssgenome.wi.mit.edu
Conter project name: 15757
Center project name: 15757
Center clone name: 956,N_15

source

1. .181607

organism="Homo sapiens Location/Qualifiers

/mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="17"

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in Submitted (07-SEP-2001) Whitehead Institute/MIT Center for Genome Research, 230 Charles Street, Cambridge, MA 02141 [USA Class of the 181607]

(C2 4 (Dases 1 to 181607)

RS Birren, B., Lintcon, J., Wusbaum, C., Lander, E., Ali, A., Allen, N., Andercon, S., Barra, M., Bestien, V., Boguslavkiy, J., Boukhgalter, B., Roccok, P., Barra, M., Bestien, V., Boguslavkiy, J., Boukhgalter, B., Erom, A., Comarata, J., Campopiano, A., Cheny, J., Cook, A., Cook, A., Cook, P., Debrellano, K., Deary, S., Collymore, A., Cook, A., Cook, P., Berra, N., Deary, S., Dodge, S., Fauc, S., Fauc, S., Grand, P., Gren, M., Cook, A., Cook, A., Cook, A., Cook, P., Cook, P., Cook, P., Cook, P., Cook, A., C
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                                                                                                                                                                                                                                                                                                         Submitted (10-JAM-2002) Miltehead Institute/MIT Center for Genome Research, 320 Charles Exrect, Cambridge, MA 0214, USA. On Jan 10, 2002 this sequence version replaced gi:15487420. All repeats were identified using RepeatMadker: smit, A.F.A. & Green, P. (1996-1997).
                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Direct Submission
Center: Whitchead Institute/ MIT Center for Genome Research Center code: WIBR
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/rpt_family="MLTIG1"
20583. .20603
/rpt_family="AT_rich"
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/rpt_family="L1M2"
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/rpt_family="LiN1"
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171. .411
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2523. .12786
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ement/'^^
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                                                                                                                                                                                                                                                                                                                       Submitted (03-FEB-2003) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                              Paulieni, Banerjei, J., Wyers, G.S.A., Nelson, K.B., Seshadri, R., Read, T.D., Fonte, D.B., Exten, J.A., Gill, S.R., Heddelborg, J.F., Tettedini, Dodson, R.J., Umayam, J., Erinkso, L., Beann, M., Guerre, J., Goldon, R.J., Umayam, J., Brinkso, L., Beann, M., Daugherty, S., Deboy, R.T., Durxin, S., Kolonay, J., Wadupu, R., Walton, M., Wamathevan, J., Tran, B., Upcon, J., Hansen, T., Shotty, J., Monarli, H., Uttershack, T., Asdune, D., Kecchum, X.A., Dougherty, B.A.
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Enterococcus faecalis V583, section 10 of 11 of the complete
                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                             and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Fraser, C.M.
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Enterococcus faecalis V583
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complement(24666. .24713)
/rpt_family="MADE1"
    complement (94. . .2229)

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complement(24285. .
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complement(23398..23
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22874. .23032
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                                                                                                                                                                                       /organism="Enterococcus
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/strain="V583"
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; pred. No. 92;
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/locus_tag="RB2859"
complement (4728. .4907)
/locus_tag="RB2859"
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VAFDKTQIQNVLNDDGTINKEKLTTWVTQLETTYGSANQPVLFTDVHGTTRRFKNNGS
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/product="BrK/Ybis/Yof8/YnhG family protein, putative"
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/product="4-oxalocotonate tautomerase,
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ENTHRFVVLHRGIVSTMERFVAYLTEYYKGAFPTWLAPIQATIIPVSVEAHSEYAYEI
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DQIKDBFKRTLBLMVAVYADFNITDYRFRLSYRDPNNTDKYFDDDAMWEKAQAMLKAA
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/transl_table=
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/gene="thrs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPFTTARGLKSDKFSIAAKTGTAETQATDANGVNHTTVNSNLVAYAPYENDEIAISVV
LPHLNDBASKENQTIAKEVLEAYMENYKK"
                                                                                                                                                                                                                                                                                                                                             db_xref="GI:29344795"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="identified by match to PFAM protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'locus tag="EF2860"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MSIHITFPDGAVKPFDSGITTFDVAKSISNSLAKKALAGKFNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          locus_tag="EF2858"
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/protein_id="AAO82549,1"
/db_xref="GI:29344792"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MPFVHVELIEGRTHEQLTNMVKDITEAVSKNAGAPKENIHVIVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _table=11
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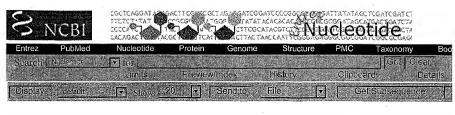
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HLDGIDFDDE YAZVGNOTEPONISSE T WILDALRANLSHIKI ITYVIIGFAANISSA
NEQMSSI IDYAMNEYYSTMIEPOLIAGMPASRLGASA VEVGVNONLAAQYAKRTKABOY
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SP:P8356, FID:32391, FID:32398, GB:X59372, GB:X15506,
SP:P17482, SP:P28356, FID:32391, and FID:32398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (10676.
                                                      enndtnilgflgmngndfffraqskqmaanggtgtvgffrvsfqgavritdargn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=\overline{\ } similar to GF:23094472; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (9611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIYLMYNLPGKDSSAYISAATQELYGRKTNYSPTVPTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTPXTVMYVEVNNHDFNNVGKYTLAGTNQPAFDMGIIFAANINYDTVNKKPYLYLNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8388. .9332
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similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (6664. 7527)
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LIDGKXLVTTPULTGRYNKGYDATVFGFHTILLKTTUVNLBGQMLDGSRYSVDVKYVGYDA
VYMCGYVTQLGLHDSDHKKIDKYGDXEBAKTDAGSNGCLHTGGTSVSKLFUVSKDGNYGV
                                                                                                                                                                                                                                                                                                     /protein_id="AA082556.1"
/db_xref="GI;29344799"
                                                                                                                                                                                                                                                                                                                                                                                                  product="conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl
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'note="gimi":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MGHQLSTHFFNKKTGIISTFLSLILLVGGLLFALPAFEVQAAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="endo-beta-N-acety1glucosaminidase"
/protein_id="AAO82555.1"
/db_xref="GI:29344798"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="EF2862"
7649. .8230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/product="aminoglycoside 6-adenylyltransferase"
/protein_de=#AA002553.1"
/db_xref="GI:29344796"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIYGHIYDDAPGEPDKPVDYGEEV"
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.11395)
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54.1"
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☐1: AX028511. Sequence 14 from ...[gi:10189694]

Links

LOCUS AX028511 31 bp DNA linear PAT 16-SEP-2000 DEFINITION Sequence 14 from Patent WO0042216.

DEFINITION Sequence 14 from Patent WO0042216. ACCESSION AX028511

VERSION AX028511.1 GI:10189694

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kusk, P.

TITLE Genetic predisposition

JOURNAL Patent: WO 0042216-A 14 20-JUL-2000;

OSTEOMETER BIOTECH AS (DK) ; KUSK PHILIP (DK)

FEATURES Location/Qualifiers

source 1..31

/organism∞"Homo sapiens" /mol type="unassigned DNA"

/db xref="taxon:9606"

ORIGIN

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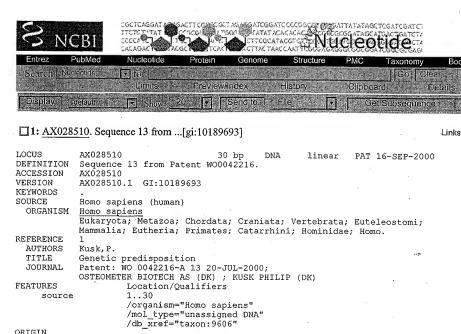
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